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/db_xref="taxon:4577"

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 comparative analysis of the plant cellulose synthase (CesA) gene
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SCCTIG	ATGGC	ATGGC	TGGTG	TGGTG	AGCGTC	ACGTC	AGCTG		CAGTA	CTGTT	CTGCT	ACAGGA 	TTATG	TTATE	TAAGG	TAAGC	GTCAA 	AGTAT	AGTAT	AATCAG	ATCAC	TIGCCT	GAAAG 	GATTG	AAGAG	CATCA	TCTTT
AAATGO	CACACC	CACACC	TCACAG	TCACAC	TGAAA	TGAAA?			CAACA	GCAAG	GAGTG	TGCAAA	ACCAG	ACCAG	CCCAAI	CCCAA	AAGCAA AAGCAA	TGTTCC	TGTGCC	TGAGAZ	TGAGA	ATTTG1 TTTTG1	TCTTT1 	AACTGA 	GCACGC	16000 	TGAAA1 GGAAA1
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Zea mays

Eukaryots, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryots, Wanoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

Dhugga, K.S. and Helentjaris, T.G.

Maize cellulose synthases and uses thereof

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PIONEER HI-BRED INTERNATIONAL, INC. (US)
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Holland, N., Holland, D., Helentjaris, T., Dhugga, K.S., Xoconostle-Cazares, B. and Delmer, D.P. A comparative analysis of the plant cellulose synthase (CesA) gene
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Dhugga,K.S. and Helentjaris,T.G.
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Zea mays cellulose synthase-5 (CesA-5) mRNA, complete cds. AF200529 GE:96228R1
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/note="identified and isolated from the maize genome
/database cDNA collection of Pioneer Hi-Bred International,
Inc"
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Helentjaris,T., Dhugga,K.S.,
Xoconostle-Cazares,B. and Delmer,D.P.
A comparative analysis of the plant cellulose synthase (CesA) gene
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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Avenue, Johnston, IA 50131,
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GGAACGAGCAGTTCTGGGTGATCGGGGGCATCTCCGCGCACCTCTTCGCCGTGTTCCAGG
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Plant Physiol. 123 (4), 1313-1324 (2000)
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Dhugga,K.S. and Helentjaris,T.G.
Direct Submission
Submitted (01-NOV-1999) Agronomic
International, Inc., 7250 NW 62nd
Location/Qualifiers
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78	TCCCTACAGAATGGTCATTGTT	GGTTGGTTGTTCTAAGCATCTTCCTGCACTACCG 937
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998	TTGGTTTGCTTATCCTGGATA	ATCAGTTCCCGAAGTGGTTTCCAATCAACCGGGA 1057
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H	TGCTGTTGACATATTTGTCAG	GACCCCTTGAAGGAGCCACCTATCGTCACTGC 117
303	CCTGTTGATATTTTGT	SCAATGAAGGAGCCTCCTCTTGTCACTGC 136
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	ATCTGATGACGGAGCTTCAAT6	GAGTTTGC 129
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478	SCATTGAAAGTCCCCGAG	SGATCATGCAAGATGGCACACCATGGCCAGGAAA 1537
693	GGCACAAAAGTTCCCGAGGA	SGATCATGCAAGATGGTACACCTTGGCCTGGGAA 1722
538	CAATACCAGGGATCATCCTGG	TTCAGGTTTTCCTTGGTCACAGTGGTGGCCTTGA 1597
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843	CAACATCACAAGAAGGCTG	scacirgircgigiarcaccigiccirac 190
718	TAATGGACAATACATGTTGAAT	77
903	SGCCAATACATGTTG	STGACCACTACATCAATAATAGCAAGGCTCT 196
778	CCGAGAAGCTATGTGCTTCCT	ATCCAAACCTAGGTCCGCAAGTCTGTTATGTGCA 1837

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Laosinchai, M., Cui, X. and Brown, R.M. Jr.
A full length cDNA of cotton cellulose synthase has high homology
with the Arabidopsis RSWI gene and the cotton CelAl gene (Accession
No. AF200453) (PGR 00-002)
Plant Physiol. 122 (1), 291 (2000)
2 (bases It o 3723)
Y. Itoh, T., Cui, X. and Brown, R.M. Jr.
Immunogold Labeling of Rosette Terminal Cellulose Synthesizing
Complexes in a Vascular Plant (Vigna angularis)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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Laosinchai, W. and Brown, R. M. Jr.
Direct Submission
Submitted (11-MAY-1999) Botany, University of Texas at Austin, 24th Street, Austin, TX 78713, USA
4 (bases 1 to 3723)
Laosinchai, W., Cui, X. and Brown, R. M. Jr.
Direct Submission
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1400 CTTTTCCCTGATGTGGGTTCGTATCGATCCATTCACCCGGGTCACTGGCCCTGATAT
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Submitted (17-NOV-1999) Molecular Genetics and Microbiolog
Submitted (17-NOV-1999) Molecular Genetics and Microbiolog
University of Texas at Austin, Austin, TX 78712, USA
Sequence update by submitter
On Nov 17, 1999 this sequence version replaced gi:5081778.
                                    CTTCACTGTCACCTCAAAGGCTAATGACGAAGAAGGCGACTTTGCTGAGCTCTACATGTT
                                                                                                     CAAGTGGACGACGCTTCTCATCCCTCCGACGACCATTTTGATCATTAACATGGTTGTTGT
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/cultivar="Texas marker-1"
/db_xref="taxon:3635"
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AF150630.2 GI:6446576
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                                                 /product-"cellulose synthase catalytic subunit"
/protein_id="AAD39534.2"
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Spermatophyta; Majpolantae; streptophyta; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 3682)

AriollyT., Peng,L., Betzner,A.S., Burn,J., Wittke,W., Herth,W.,

Camilleri,C., Hofte,H., Plazinski,J., Birch,R., Cork,A., Glover,J.,

Redmond,J. and Williamson,R.E.

Molecular analysis of cellulose biosynthesis in Arabidopsis

Science 279 (5351), 717-720 (1998)
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Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B)
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Submitted (29-SPB-1997) Plant Science Centre, Australian National
University, Acton, Camberra, ACT 200, Australia
Location/Qualifiers
1. 3682
/organism="Arabidopsis thaliana"
/cultivar="Columbia"
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GGUYDASTDILADEBALUNDERROPLSKWSTPSERINDYRMIGHUYILGUEFLIKE
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QQ	892	TGAAAGAGGT	GATATTGATGCCAGCACAG	m
oy op	804	GAAGACGCTTTACTGAATGATG GATGAGCTCTGCTGAATGACG	GCCAGCCTCTATCTAGAAAAGTCCCCATTGCT 863 	, e
οy	vo :	TCCTCCAAAATAAATCCCTACA	923	
д	0	TCATCACGGATCAATCCTTACA	ATGCTGCGGCTTGTTATCCTTTGTCTC 106	8
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QQ	1129		CTGGATTTTGGATCAGTTTCCCAAGTGGTTT 118	88
δλ	1044	CCAATCAACCGGGAGACCTACC	AGACTGGCTTTAAGGTATGACCGAGAAGGTGAA 110:	33
qq	1189	CCTGTGAACCGTGAAACCTACG	3 124	8
Qy Db	1104	CCGTCTCAGTTGGCTGCTGTTG	MTTGTCAGTACAGTCGACCCCTTGAAGGAGCCA 116: 	£ 8
δ	9	CCTATCGTCACTGCCAACACTG	3 122	3
qq	1309			89
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οy	28	ACTICAGAGITIGCIAGGAAAT	CCATTGRAAGAAGTATGACATTGAACCCAGA 134:	ñ
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Q	1489	GCACCAGAATGGTACTTTGCTG	154	80
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Qy	1584	AGTGGTGGCCTTGATACTGAGG	GAGCTCCCCGTTTAGTTTATGTCTCTCGTGAA 1643	m
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δy	1644	AAGCGTCCTGGGTTCCAGCACC	AAGGCTGGTGCCATGAATGCCCTTGTTCGTGTC 1703	m
QQ	1789	AAGCGACCAGGATTCCAGCACC	184	æ
δλ	70	TCAGCTGTCCTTACTAATGGAC	92	
අධ	1849	TCAGCAGTICTTACCAATGGAC	190	
δλ	76	AACAGCAAGGCTGTCCGAGAAG	82	ლ 9
g	1909	AACAGCAAAGCCTTAAGAGAAG	196	8

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Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Walliamson, R.E., Peng, L., Arioli, A. and Betzner, A.S. Manipulation of cellulose and/or beta -1,4-glucan Patent: WO 9800549-A 9 08-JAN-1998;
WILLTAMSON RIGHAND EDWARD (AU); PENG LIANGCAI (AU) ANTONIO (AU); UNIV AUSTRALIAN (AU); BETZNER ANDREACOMMW SCIENT IND RES ORG (AU)
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DUNT 963 a	y Match 46.2%; Score 1673.6; Local Similarity 71.4%; Pred. No. 0; hes 2347; Conservative 0; Mismatches	30 TCGGTGCGGGTTGGATCGCTCTGCCGCCCATGGACGCGGACGCGGACGCCGTGAAGTCC	190 TCGGTGTTGGAAGCAACTAAGTGAAATGGAATCCGAAGGAGAAACCGCGGGAAAGCCG	90 GGGAGGCACGGGGACGTGTGCCAGATCTGCGGCGGGCTGGGCACGCAC	150 GACGGCGACGTCTTCACCGCCTGCGACGTCTGCCGGTTCCCGGTCTGCCGCCCTAC		210 GAGCACGAGCGCAAGGAGGCACCCAGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGC	270 CACAGAGGGAGCCCAGCGATCCGCGGGGAGGAAGGAGGGGACACACAGATGATGCCGATGATGTT		490 ACTGTTGAGTTCAACTACCCT	387 AGGATGCGCAGCTGGCGCATGAACACCGGGGCAGTGGCCAATGTTGGCCACCCCAAGTAT	GACAGTGGCGAGATCGG	592 GATAAAGAGGTCTCTCACAATCATCTTCCTCGTCTCACGAGCAGGAGGAG	507 CCTTCAGTCACCAACAGCCAGATGTCAGGAGAAATCCCTGGAGCTTCGCCTGATCATCAC 	567 ATGATGTCCCTACGGGAACATCAGCAGACGTGCTCCGTTTCCCTATGTGAATCAT 	624 TCACCAAATCCGTCAAGGGAGTTCTCCGGCAGTATTGGGAAAGTGTTGCCTGGAAAGAGAGA 1111111	684 GITGATGGCTGGAAAATGAAGCAGGACAAGGGTGCGATTCCCATGACTAATGGGACAAGC	1 +		804 GAAGACGCTTTACTGAATGATGAACTCGCCAGCCTCTATCTA	S64 TCCTCCAAAATAAATCCCTACAGAATGGTCATTGTTCTGCGGTTGGTT	
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

CE 1 (bases 1 to 3614)

RAIliamson, R. E., Pengil., Arioli, A. and Betzner, A. S.
Manipulation of cellulose and/or beta -1,4-glucan

RAILIAMSON RICHARD EDWARD (AU); BETZNER ANDREAS STEFAN (AU);
COMMW SCIENT IND RES ORG (AU)

COMMW SCIENT IND RES ORG (AU)
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QQ	250		
δŏ	150	GACGGCGACGTCTTCACCGCCTGCGACGTCTGCCGCTTCCCGGTCTGCCGCCCCTGCTAC 20	
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Q	370	GAGTATGAGAGGAAAGATGGGAATCTTGTCCTCAGTGCAAAACCAGATACAAGAG 429	
QY Db	270	CACAGAGGGAGCCCAGCGATCCGCGGGGAGGAAGGCGACCACACACTGATGCCGATGATGGT 329	
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6. P. G.	330	AGTGACTTCAACTACCTGCATCTGGCACTGAGGACCAGAACAGAAGATGCTGC 386	
δ	387		
qq	532		
λō.	447	GACAGTGGCGAGATCGGCCTCTCCAAGTATGACAGTGGAGAGATCCCTAGGGGATACGTC 50	
g	592	GATAAAGAGGTCTCTCACAATCATCTTCCTCGTCTCACGAGCAGACAAG 640	
ŏ	507	CCTTCAGTCACCAACAGCCAGATGTCAGGAGAATCCCTGGAGCTTCGCCTGATCAC 566	
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οy	267	ATGATGTCCCTACGGGGAACATCAGCAGACGTGCTCCGTTTCCCT	
g	682	TCTGTATCTTCTACTATCGCTGGGGGAAAGCGCCTTCCCTATTCATCA	
ò	624		
QQ	742		
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qq	802	GTTGATGGCTGGAAAATGAAGGAAGAAGAATACTGGTCCTGTCAGCACG 852	
QY	744	ATTGCTCCTCTGAAGGTCGGCAGCTACTGACATCGATGCATCTACTGAATACAACATG 803	
С	853		
δ	804		
ΩD	910	GATGAGGCTCTGCTGAATGACGAGGGAGGCAGCTTCTGTCAAGGAAAGTTTCAATTCCT 969	
δ	864	TCCTCCAAAATAAATCCCTACAGAATGGTCATTGTTCTGCGGTTGGTT	
q	970		•
λŏ	924	TICCIGCACTACCGICICACAAATCCIGIGGGIAATGCATACCCACIGIGGCITITAICT 983	
g	1030		σ.
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2057 1343 2049 2289 1403 1463 1583 1703 1609 1763 1943 2109 2117 2237 GAGCICCCCGTTTAGTTTATGTGTCTCGTGAA 1643 GCTTCCTAATGGATCCAAACCTAGGTCCGCAA 1823 ACAAAAAGAAATCAGGCAGGCATACTGACTCA 2229 ATGGTGGTGTTCCTCAGTCCTCCACAGAA 2297 GAGCCTGGAGAAGCGATTTGGACAGTCTGCT AACTTGAGGGCCTTGACGCATTCAAGGACCA TCCATTCTTGCTGTTGATTATCCCGTGGACAAG GCTTCAATGCTGACTTTTGACGCATTGGCTGAG CCATTTGTGAAGAAGTATGACATTGAACCCAGA ATTGATTACCTGAAAGACAAAGTCCAGCCTTCA CATCCTGGAATGATTCAGGTTTTCCTTGGTCAC **TGTTGAATCTTGATTGTGATCACTACAAC** AACTTGAGAGGTTTAGATGGGATTCAAGGACCT ACAGAACAGCTATCTATGGTTATGAGCCCCCA TCTTGGCATCACTATGTGGGGGCAAGAAGAAG ATAAGAAAAGTCGAACAAGCATGTGGACAGT TAGAGGAGGGTGTTGAAGGTGCTGGGTTTGAT TGAGCTTAGAGAAGAGATTTGGCCAGTCAGCA AAGAATTCCAAAGCTAAGAAAG GCATTTGTTGCCTCCACTCTGA TCAGCAGTTCTTACCAATGGAC AACAGCAAGGCTGTCCGAGAAG AACAGCAAAGCCTTAAGAGAAG GTCTGTTATGTGCAGTTCCCAC AACAGGAACACTGTCTTTTTG AATCGTAATACCGTGTTCTTTG GTTTATGTGGGAACTGGTTGTG 2050 GTATATGTCGGAACTGGATGTG ATTAAGG------CGAAGAAGC ATAAAAGTAAAACACAAGAAGC GCAAGCAAGTCAAAGAAAAGGA TCTGTTCCAGTATTCAATCTCG 2230 ACTGTTCCTGTATTCAACCTCG GATGAGAAATCAGTTCTCATGT CCGTGGCCTGGAAATAATACAG AATGGTGGACTTGATGCAGAGG AAGCGTCCTGGGTTCCAGCACG AAGCGACCAGGATTCCAGCACC TCAGCTGTCCTTACTAATGGAC GATGAAAAGGCGCTCTTAATGT CCCCTTGTGACAGCCAACACAG GCTCCCGAGTTTTACTTTGCC GCACTTGTTTCCAAAGCCCTAA AGTGGTGGCCTTGATACTGAGG GTCTCTTGCTATGTATCTGAT GIGTCCTGTTATGTTTCTGATC ACATCAGAGTTTGCTCGTAAA TTTGTTAAAGACCGCCGGGCC GCCCTAGTTTCTAAGGCATTG1 CCATGGCCAGGAAACAATACCI CCTATCGTCACTGCCAACACT ACTTCAGAGTTTGCTAGGAAA 1810 2238 1164 1270 1224 1330 1284 1390 1344 1450 1404 1510 1464 1570 1524 1630 1584 1690 1644 1750 1704 1764 1870 1824 1930 1884 1990 1944 2004 2110 2058 2170 2290 В O.Y D Q QQ o O g q 셤 Q g g g qq 90 90 90 90 oy Oy δ g δ QΥ οχ ò ò QY οy Ω ò δ

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                                                                                                                                       2530 ATGCATGCCCGTGGATGGCGATCCATTTACTGCATGCCTAGCTTCCAGCTTTCAAGGGT 2589
                                                                               GGAACTGAGATTGGTTGGATCTATGGATCTGTCACAGAAGATATTCTTACTGGATTCAAG
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2710 TICTTGAGAGGTTTGCGTATGTGAACACCACCATCTACCCTATCACCTCCATTCCTCTT
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                                               CCATTCCTCAAGGGTCTTATGGGCAGGCAAAACCGCACGACGACGATTGTCATCGTCTGG
                                2298 TCTCTTTTGAAAGAAGCTATCCATGTCATAAGTTGTGGCTATGAGGACAAGTCTGAATGG
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/ GALD LIGE SYNTHASE-2"
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/ GALD LIGE "AAANGGWAGSHNRNEEVMIRHDCDAPVPARPTKSANGOVCOIC
GOTVGVSATGOVFVACNECAPPOVRPCYEYERKEGNOCCPOCKTRYRROKGSPRVHGD
BEEDVDDLJONEFWYGGONGKOPEWOLGODAPLSSSARHDPHHRIPRITSGOOISGE
DEASPDRISIRSPRSYUDPSVPVPVRIVDPSKDLMSYGLMSYDWWERVESRRVKOD
KNMLQOYTWXTPEARCDMGGTGSNGEDMGWNDDARLELSRIVPISSOUMERVESRRVKOD
KNMLQOYTWXTPEARCDMGGTGSNGEDMGWNDDARLELSRIVPISSUDWKSRVSSRVKOD
KNMLGOYTWYTPEARCDMGGTGSNGEDMGWNDARLELSRIVPISSULAVDFUFKENA
LITICPFFOYR ISHPVRAWAGGLMUSSYLCFWRALSMLLAOPPOWRVSTVSDDGS
AMLTFESLSFTGFARKWVPFCKKNIEPFRAPFFYFAOR IDVIKDYTUSRLA
LRYDREGESOLAPIDVFVSTVDPIKEPPLITAMTVLSILAVDCHYFURSKA
LRAMCFBMDPAALGKTTVVOFPORFOGTHUNDROHPROHPOMIOVFLGHSGGLDT
DGWBLPRLYVYSTREKRPGFOHHKRACAMNALITVSSVALLNOAYLLNOCHPTRNSKA
LRRAMCFBMDPAALGKTTVVOFPREADLEPHIVVKSCGGRRKKRKNSYMDGGIPPSTNPAS
LLKEAMCFBMDPAALGKTTVVOFPREADLEPHIVVKSCGGRRKKRKNSYMDGGIPPSTNPAS
LLKEAMUSDRLNOVLRWALGSSVLMSORKLEKRFRGOSITCHELRNSTTS
CLKERAHVISCRSEDFTSTWAGSFILLFRENGTREANITTVYPTTS
SYPLIAYCYLLDAICLLITNKFITERISSTELLERNSTGNITTVYPTTS
                       3725~\mathrm{bp} mRNA linear PLN 31-AUG-2000 cellulose synthase-2 (CesA-2) mRNA, complete cds.
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RIPPTVLVINJVGWYAGISYAINSGVOSWGPLFGKLFFSIWVIHLYPFLKGLWGRQN
RIPTIVIVNSILLASIFSLLWVKIDPFISPTQKAAALGQCGVNC"
807 c 955 g 1041 t
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/note="identified and isolated from the maize genome
database cDNA collection of Pioneer Hi-Bred International,
Inc"
                                                                                                                                                                                                                                                                                                           Xoconostle-Cazares, B. and Delmer, D. P.
A comparative analysis of the plant cellulose synthase (CesA) gene family
                                                                                                                                                                                                   Tracheophyta;
ceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 CTGCCAGATTTGTGGCGACACTGTTGGCGTTTCAGCCACTGGTGATGTTTTGTTGCTGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Traits, Pioneer Hi-Bred
Avenue, Johnston, IA 50131,
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                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trache
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
clade, Panicoldeae, Andropogoneae, 2ea.
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                                                                                                                                                                                                                                                                                                Dhugga, K.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Pred. No. 3.7e-267;
0; Mismatches 966;
                                                                                                                                                                                                                                                                      1 (bases 1 to 3725)
Holland, N., Holland, D., Helentjaris, T.,
                                                                                                                                                                                                                                                                                                                                                                                                Physiol. 123 (4), 1313-1324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 3725)
Dhugay.K.S. and Helentjaris,T.G.
Direct Submission
Submitted (01-NOV-1999) Agronomic Tr
International, Inc., 7250 NW 62nd Av
Location/Qualifiers
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179. .3403
/gene="CesA-2"
/note="CESA-2"
                                                                                                GI:9622875
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Best Local Similarity 66.8%;
Matches 2147; Conservative
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                                                 Zea mays cel
AF200526
AF200526.1
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                          AF200526
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AF200526
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1489

1549 1650 1669

oy B	173 358	CGACGTCTGCCGCTTCCCGGTCTGCCGCCCTACGAGCACGAGCGCAAGGAGGCAC 232	
Qy	233	CCAGGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGCCACAGAGGAGCCCAGCGATCCG 292 	
Q _Y	293	CGGGGAGGAAGGCGACACTGATGCGGATGATGAGTGACTTCAACTACCCTGCATC 352 	
Oy Dp	353 538	TGGCACTGAGGACCAGAAGAGATTGCTGACAGGATGCGCAGCTGGCGCATGAACAC 412	
QY	413	CGGGGGCAGTGGCCACCCCCAAGTATGACAGTGGCGAGATCGGCCTCTCCAA 472 	
Oy Dp	473 635	GTATGACAGTGGAGAATCCCTAGGGGATACGTCCCTTCAGTCACCAACAGCCAGATGTC 532	
Qy Db	533 652	AGGAGAAATCCTGGAGCTTCGCCTGATCATCACATGATGTCCCCTACGGGGAACATCAG 592 	
Qy Dp	593	CAGACGICCTTTCCTAIGTGAAICATTCACCAAAICCGICAAGGGAGITCIC 649	
Q Dp	650	CGGCAGTATTGGGAATGTTGCCTGGAAAGAGAGTTGATGGTGGCTGGAAAATGAAGCAGGA 709 	
Qy Dp	710	CAAGGGTGCGATTCCCATGACTAATGGGACAAGCATTGCTCCCTCTGAAGGTCGGGCAGC 769 	
Oy Dp	770	TACTGACATGGATGCATCTACTGAATACAACATGGAAGACGCTTTACTGAATGATGAAAA 829 	
Qy Db	830 931	TCGCCAGCCTCTATCTAGAAAAGTCCCATTGCTTCCTCCAAAATAAAT	
Qy Dp	890 991	GGTCATTGTTCTGCGGTTGGTTGTTCTAAGCATCTTCCTGCACTACCGTCTCACAAATCC 949	
δ O	950 1051	TGTGCGTAATGCATACCACTGTGGCTTTTATCTGTTATATGTGAGATTTGGTTTGCTTT 1009	
oy Op	1010	ATCCTGGATACTGGATCAGTTCCCGAAGTGGTTTCCAATCAACCGGGGAGACCTACCT	
Qy Db	1070	TAGACTGGCTTTAAGGTATGACCGAGAAGGTGAACCGTCTCAGTTGGCTGCTGTTGACAT 1129 	
Q Dp	1130	ATTIGECAGTACAGTCGACCCCTEGAAGGAGCCACCTATCGTCACTGCCAACACTGTGCT 1189	
Qy Db	1190	ATCCATTCTTGCTGTTGATTATCCCGTGGACAGGTCTCTTGCTATGTATCTGATGACGG 1249 	

TGGTCACAGTGGTGGCCTTGATACTGAGGGTAA 1609 TCGTGTCTCAGCTGTCCTTACTAATGGACAATA 1729 CATCAACAACAGCAAGGCTGTCCGAGAAGCTAT 1789 TCCGCAAGTCTGTTATGTGCAGTTCCCACAAAG 1849 GGGTCCAGTCTATGTGGGAACAGGATGCTGTTT 2070 CAGTICIGITCCAGIATTCAATCTCGAAGACAT 2146 TGATCATGAGAAATCACTTCTCATGTCTCAAAT 2206 TCCAATCTTCATTGCATCCACCTTTATGACTCA 2364 AGGACCAGTTTATGTGGGAACTGGTTGTGTTTT 1969 GCC---CCCAATTAAGGCGAAGAAGCCAGGTTT 2026 GAAGGCAAGCAAGTCAAAGAAAGGAGCTCAGA 2086 ATGGGGAACTGAGATTGGTTGGATCTATGGATC 2386 GGCTGAGACTTCAGAGTTTGCTAGGAAATGGGT TCCTGTTTTGACTGAGCTGATCTGGAACCTAA ACCAAGAGCTCCAGAATTTTACTTTGCTCAAAA TGGCACACCATGGCCAGGAAACAATACCAGGGA AGAATCTCTTTTGAAAGAAGCTATCCATGTCAT *NTATGCAAACAGGAACACTGTCTTTTTGATAT* ACCCAGAGCTCCCGAGTTTTACTTTTGCCAGAA GCCTTCATTTGTTAAAGACCGCCGGGCCATGAA GATAAATGCCCTAGTTTCTAAGGCATTGAAAGT PCGTGAAAAGCGTCCTGGGTTCCAGCACCACAA AGCAGCATTTGTTGCCTCCACTCTGATGGAATA ACCATTTGTGAAGAAGTATGAG 1471 AATAGATTACCTGAAGGACAAA 1531 GAGAGAGTATGAAGAATTCAAA 1490 CCCCCAGGAAGGATGGATCAT GTGCTTCCTAATGGATCCAAAC 1891 GTGCTTCATGATGGATCCAGCT 2011 CAACATGAAAGGTCTAGATGGC ||| || || || || 2071 CAATAGGCAGGCTTTGTATGG CTTGGCATCACTATGTGGGGGG GAGCTTAGAGAGAGATTTGGC 2305 GAAATTGGAGAAACGCTTTGGT TGGTGGTGTTCCTCAGTCCTCC AAGTTGTGGCTATGAGGACAAG AATTGATTACCTGAAAGACAA GAGAGAATATGAAGAATTTAAJ 1711 TGAATTACCACGTCTTGTCTA GAAGGCTGGTGCCATGAATGC 1730 CATGTTGAATCTTGATTGTGA 1951 ATTTGATGGCATTGACTTGCAC TAACTTGAGGGGCCTTGACGG 1970 CAACAGAACAGCTATCTATGG 2131 CATTGTTGTTAAGAGCTGCTG TAAGAAAAGTCGAACAAGCA 2147 AGAGGAGGGTGTTGAAGGTGC AGGTGGCATACCACCTTCAAC 1411 TCCCTTTTGTAAGAAGCACAA TCATCCTGGAATGATTCAGGT 1651 CCATCCTGGCATGATTCAGGT TGAGCTCCCCGGTTTAGTTTA 1771 GAAGGCTGGTGCAATGAATGC GTTTGATGGGATTGATAGGAA TCAAAGCCGTATTATGAAGAG 2251 CGAGGAGGGTATTGAAGGT 1310 1370 1430 1550 1610 1670 1790 1850 1910 2027 2087 2191 2207 2267 2365 2327 q QΥ g οy Q QY Db QY Db Q Db OY Db O D οy 염 δy g g S δ qq δ g δ g ογ g ò g ŏ g Q δ ò

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GDSVGVSATGDVFVACNECAFPVCRPCYEYERKEGNQCCPQCKTRYKRQKGSPRVHGD
EDEEDVDDLDNEFNYKQGSGKGPEWQLQGDDADLSSSARHEPPHRIPRLTSGQQISGE
                                                                                                                                                                                                                                                                                                                                                                   /note="identified and isolated from the maize genome database cDNA collection of Pioneer Hi-Bred International,
                                                   1 (bases 1 to 3752)
Valolland, N., Holland, D., Helentjaris, T., Dhugga, K.S.,
Xoconostle-Cazares, B. and Delmer, D. P.
A comparative analysis of the plant cellulose synthase (CesA) gene
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Zea.
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Johnston, IA 50131,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 CCGCGCCATGGACGCGGACGCGGACGCCTGAAGTCCGGGAGGCACGGGGCCGGGGACGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               986;
                                                                                                                                                                                                                                                            Traits,
                                                                                                                                                                                                                                                                             Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1373; DB 8;
Pred. No. 3.5e-260;
0; Mismatches 986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="cellulose synthase-1"
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/db_xref="GI:9622874"
                                                                                                                                               Physiol. 123 (4), 1313-1324 (2000)
                                                                                                                                                                                                2 (bases 1 to 3752)
Dhuggar K.S. and Helentjaris, T.G.
Direct Submission
Submitted (01-NOV-1999) Agronomic Tr
International, Inc., 7250 NW 62nd Av
Location/Qualifiers
e 1. 3752
                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/db_xref="taxon:4577"
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/gene="CesA-1"
/note="CESA-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="CesA-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.9%;
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Matches 2130; Conservative
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                                                                                                                               TTGCATGCCCAAGCGCCCAGCTTTCAAGGGATCTGCCCCCATCAATCTTTCAGATCGTCT
                                                                                                                                                   CTTATGGTATGGCTACGGAGGGCGCCTCAAGTTCCTGGAGAGATTCGCTTACATCACAC
                                                                                                                                                                                                                                                                                                                                                   CACCATTTACCCACTAACCTCTCTCCCGCTTCTAGTCTATTGTATATTGCCTGCTATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2747 TGCGCTCTTCCTTTCAATTTTCGCCACTGGTATCCTTGAGATGAGGTGGTGGTGGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTGACGAGTGGTGGAGGAATGAACAGTTCTGGGTCATTGGAGGTATCTCTGCACATCT
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Zea mays
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çy GD	533	AGGAGAAATCCCTGGAGCTTCGCCTGATCATCATGATGTCCCCTACGGGGAACATCAG 592
oy Ob	593	CAGACGIGCICCGTITCCCTAIGIGAATCATICACCAAATCCGICAAGGGAGIICTC 649
Qy Db	650	CGGCAGTÀTTGGGAATGTTGCCTGGAAAGAGAGTTGATGGCTGGAAAATGAAGCAGGA 709
oy Op	710	CAAGGGTGCGATTCCCATGACTAATGGGACAAGCATTGCTCCCTCTGAAGGTCGGGCAGC 769
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Qy Db	830 938	TCGCCAGCCTCTATCTAGAAAAGTCCCCATTGCTTCCTCCAAAATAAAT
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Oy Ob	1070	TAGACTGGCTTTAAGGTATGACCGGGAAGGTGAACCGTCTCAGTTGGCTGCTGTTGACAT 1129
Qy Dp	1130	ATTGECAGTACAGTCGACCCCTTGAAGGAGCCACCTATCGTCACTGCCAACACTGTGCT 1189
Oy Db	1190	ATCCATTCTTGCTGTTGATTATCCCGTGGACAAGGTCTCTTGCTATGTATCTGACGG 1249
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Qy Dp	1310 1418	ACCAITIGTGAAGAAGTATGACAITGAACCCAGAGCTCCCGAGTTTTACTTTTGCCAGAA 1369

1849 2206 2326 1669 1969 AAGATGCACGCAAGAGGCTGGCGTTCAGTCTA 2446 1609 2017 2077 CC---CCCAATTAAGGCGAAGAAGCCAGGTTT 2026 GGATCTGCCCCCATCATCTTCAGATCGTCT 2506 1777 CCTATTTTCATTGCATCCACCTTTATGACACA 2371 TCGTGTCTCAGCTGTCCTTACTAATGGACAATA GCCTTCATTTGTTAAAGACCGCCGGGCCATGAA CGTGAAAAGCGTCCTGGGTTCCAGCACCACAA PCCGCAAGTCTGTTATGTGCAGTTCCCACAAAG ATATGCAAACAGGAACACTGTCTTTTTGATAT ATATGCTAATCGGAACATAGTTTCTTTGATAT CCTGTTTTGACTGAAGCTGATCTGGAGCCAAA AAGGCAAGCCAAGTCAAAGAAAAGGAGCTCAGA AGTTCTGTTCCAGTATTCAATCTCGAAGACAT TETTCAGCTCCCATCTTCAATATGGAAGACAT GATGATGAGAAATCAGTTCTCATGTCTCAAAT GCAGCATTTGTTGCCTCCACTCTGATGGAATA GAATCTCTTTTGAAAGAAGCTATCCATGTCAT IGGGGAACTGAGATTGGTTGGATCTATGGATC AAAATGCATGCAAGGGGCTGGCAATCTA CATCAACAACAGCAAGGCTGTCCGAGAAGCTAT GATAAATGCCCTAGTTTCTAAGGCATTGAAAGT ATCAATGCCCTTGTTGCCAAAGCACAGAAAGT TGGTCACAGTGGTGGCCTTGATACTGAGGGTAA CAACATGAAAGGTCTGGATGGC CAGTTGTGGATATGAGGACAAA 2387 IGTCACAGAAGATATTCTTACT TCTTCTCAATGTGGATTGCGAC ATTTGATGGCATTGACTTGCAC **AAGTTGTGGCTATGAGGACAAG** AGTAACGGAGGATATTCTGACT 2447 ITGCATGCCCAAGCGCCCAGCT GTGCTTCCTAATGGATCCAAAC CTTGGCATCACTATGTGGGGGC TAAGAAAAGTCGAACAAGCAT TCAAAGCCGTATTATGAAGAGA AGAGGAGGTGTTGAAGGTGCT GAGCTTAGAGAGAGATTTGGC TGGTGGTGTTCCTCAGTCCTCC GCCTGAAGAGGGGTGGACCATG TGAGCTCCCCCGTTTAGTTTAT GTTTGATGGGATTGATAGGAAT 1910 TAACTIGAGGGGCCTIGACGGC CAACAGAACAGCTATCTATGGT CATTGTTATTAAGAGCTGCTGT GAAATTGGAGAAACGCTTTGGT GAGAGAATATGAAGAATTTAAA CCATCCTGGCATGATTCAGGTT GAAGGCTGGTGCCATGAATGCC CATGITGAATCITGATIGIGAT AATTGATTACCTGAAAGACAAA TCATCCTGGAATGATTCAGGT1 CCCCGAGGAAGGATGGATCAT CGAAGAGGGTATTGAAGGT 1838 1478 1430 1490 1598 1658 1610 1718 1670 1778 1730 1790 1898 1850 1958 2018 1970 2078 2087 2198 2147 2258 2312 2327 2432 2492 1370 1538 1550 2027 2138 2207 2267 Q g g qq ga δ Qγ QQ δ g οy g g δ g Q g ò g g g ŏ δ g 9 ò qq οy Ω ò δ qq δ οž ŏ δ

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/organism="Arabidopsis tl/strain="CoLUMBIA"
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ANTONIO (AU); UNIV AUSTRALIA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
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Walliamson, R.E., Peng, L., Arioli, A. and Betzner, A.S.
Wantipulation of cellulose and/or beta -1,4-glucan
Patent: WO 9800549-A 5 08-JAN-1998;
WILLIAMSON RICHARD EDWARD (AU); PENG LIANGCAI (AU); ARIOLI
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Pred. No. 2.4e-254;
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Matches 2098; Conservative
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WILLIAMSON RICHARD EDWARD (AU); PENG LIANGCAI (AU); ARIOLI ANTONIO (AU); UNIV AUSTRALIAN (AU); BETZNER ANDREAS STEFAN COMMW SCIENT IND RES OFG (AL)
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g G	17	AGAGGTCTATTCTAATGTCCCA	18
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Q.y Db	2902	CCGGTATCGACACCAACTTCACT	CTCAAAGGCTAATGACGAAGAAGGCGACTTG 2961
οy	2962	CTGAGCTCTACATGTTCAAGTGG	GCTTCTCATCCCTCCGACGACCATTTTGATCA 3021
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VOYGAETGODVPVACURCAFPVCRPCYSTERKOGTOCPOCKTRFRRHESDED
BDDVDDIENERNYAGCARNKARHORHGEEFSSSRHESOPIPLLTHGHTVSGEIRTPDP
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VIOLEMBENYAGGEIEGTSGSTSSKESSSRHESOPIPLTHGHTVSGEIRTPDP
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VIILBLIILCFFLUKTTHPVKNAYPHLMLSYGLEGFSCHOPPRVYPINETY
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SUDGSAMLTEBELSETRAFAKKWPPFCKRFNEDERAPREFFSGRILDLENETY
ERRAMKREYEEFSTRAFAKKWPPFCKRFNEDERAPREFFSGRILDLENETY
GGLDDGGNELPRLIYVSREKRPGFQHHKKAGAMMALIRVSVVLTNGBYLLNVDCDHYF
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GGPVYVGTGCCFNRQALYGYDPVLTEEDLEPNIIVKSCCGSRKKGKSSKKYNYEKRG

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PPRRAFKGSAFINLSDRLNOYLKWALGSIEILLSRHOPIWYGYHGRLERLARYINT

IVYPITSIPLIAYCILPAFCLITDRFIIPEISNYASIWFILLFISIAVTGILELRWSG
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FKWTALLIPPTTVLLVNLIGIVAGVSYAVNSGYQSWGPLFGKLFFALWVIAHLYPFLK
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Manipulation of cellulose and/or beta -1,4-glucan
Patent: WO 9800549-A 11 08-JAN-1998;
MILIAMSON RICHARD EDWARD (AU); PENG LIANGCAI (AU); ARIOLI
ANTONIO (AU); UNIV ANSTRALIAN (AU); BETZNER ANDREAS STEFAN (AU)
LOCATION/QUALIFIERS
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Pred. No. 4.9e-254;
0; Mismatches 992;
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WO9800549.
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/db_xref="G1:10278352"
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/isolate="RSW1 MUTANT"
/db_xref="taxon:3702"
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CAGAGGGAGCCCAGCGATCCGCGGGGGGGAGGCGACGACCACTGATGCCGATGATGGTAG
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PLN 20-SEP-2000 Streptophyta; Embryophyta; Tracheophyta; rta; eudicotyledons; core eudicots; isicales; Brassicaceae; Arabidopsis. 2481 CCATTTACCCACTAACCTCTCCCGCTTCTAG 2661 GCAATCCTCCACGCCTGCGTTCAAGGGATCTG 2492 2781 TTGACGAGTGGTGGAGGAATGAACAGTTCTGGG 2841 |||| || |||||||||| || |||||||||| TTGAGGATTGGTGGAGGAACAGCAGTTCTGGG 2852 PATGGTATGGCTACGGAGGGCGCCTCAAGTTCC 2601 GCTTCTCATCCTCCGACGACCATTTGATCA 3021 CTCAAAGGCTAATGACGAAGAGGCGACTTTG 2961 GCCTTCTGGGTGATTGTTCACTTATACCCAT 3141 CCGCACACCGACGATTGTCATCGTCTGGGCTG 3201 GCATGCCCAAGCGCCCAGCTTTCAAGGGATCTG ACCAAGTGCTGCGGTGGGCTCTCGGTTCTGTTG GCTCACTGGAAAGTTCATGCCAGAGATTA SECTOTICCTITICAATITICGCCACTGGIATCC CTCCTACGCCATCAACAGTGGTTACCAATCAT GTGGGTTCGTGTTGATCCATT 3250 ||||| | | | | || || || TTGGGTCAGGATCAATCCCTT 3261 linear DNA 573 bp 59800549. naliana Hadiplan Magnol :102783 CTTCAC CAAGTG ||| || |CAAATG CTTCTC |||||||| CTTCTC om Pate TGATCO SGCATTO | |||||| |SACATTO ACATCAA | ||||| CTGGTT TTGGTT TGCACA CGCCCA CTTCAC GGGAAG CCCTT TGTGGC GAAGCT GAAGCT GGGCAG ATCGA TGCTAT CGTTGC TTCAG AGATC

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FKWTALLIPPTYLLVNILGIVAGVSYAVNSGYQSMGPLFOKLFFRLWYLAHLYPFLK
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IVYPITSIPLIAYCILPAFCLITDRFIIPEISNYASIWFILLFISIAVTGILELRWSG
Williamson, R.E., Peng, L., Arioli, A. and Betzner, A.S.
Manipulation of cellulose and/or beta -1,4-glucan
Patent: WO 9800549-A 08-JAN-1998
WILLIAMSON RICHARD EDMARD (AD); PENG LIANGCAI (AU); ARIOLI
ANTONIO (AU); UNIV ANSTRALIAN (AU); BETZNER ANDREAS STEFAN (AU)
COMMW SCIENT IND RES ONG (AU)
Location/Qualifiers
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                                                                                          /organism="Arabidopsis thaliana"
/strain="COLUMBIA"
/isolate="RSWI MUTANT"
/db_xref="taxon:3702"
                                                                                                                                           868 g
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1651 1659 1711 1719 1771	1831 1839 1891 1899	1951	2062 2079	2122 2139 2182 2182 2193	2242 2253 2302 2313	36	2422 2433 2482	55	2602 2613 2662 2673
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GCAACTTGGCCAGTATCTGGTT	GCAACTACGCGAGTATTTGGTT	TTGAGATGAGGTGGAGTGGTGT 	TCATTGGAGGTATCTCTGCACA		CCGGTATCGACCAACTTCAC	CTGGTATCGACACCAACTTCAC	CTGAGCICTACATGTTCAAGTG 	TTAACATGGTTGGTGTCGTTGC	rgaaccicataggcatreregc	GGGGGCGCTCTTTGGGAAGCTC		TCTTGAAAGGTCTTGGGAAGA	recreaterreratered	TTCTTCTCGCCTCCATCTTCTC	AF200532 Zea mays cellulose sy AF200532 AF200532.1 GI:962288	Zea mays. Zea mays Eukaryota; Viridiplan Spermatophyta; Magnol	clade; Panicoideae; Ai 1 (bases 1 to 3812)	Acomparative analysis	ramily Plant Physiol. 123 (4) 20398328	10938350	Dhugga, K.S. and Helent	Submitted (01-NOV-1999) International, Inc., 7	Location/Qual 13812	/organism="Ze /db_xref="tax /note="ident! database cDNA	nc" 3812	/gene="CesA-8 214. ,3498
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CISVTGILEMRWSGVAIDDWWRNEQFWVIGGVSAHLFAVFQGLLKVFAGIDTSFTVTS
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AFWVIVHLYPFLKGLVGRONRTPTIVIVWSILLASIFSLLWVRVDPFLAKSNGPLLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1340.2; DB 8; Length
Pred. No. 1e-253;
0; Mismatches 1023; Indels
/product="cellulose synthase-8"
/protein_id="AAF89968.1"
/db_xref="G1:9622888"
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ALIGNMENTS

AAS16458 standard; cDNA; 3799 BP

RESULT 1 AAS16458

AAS16458;

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Corn; ss; cellulose synthase; Cdpgs45; cesA-3; Cqrae19; cesA-9; stalk quality; improved stand; silage; pericarp; kernel hardening; handling abllity; transgenic plant.
                                                   Corn cDNA encoding cellulose synthase Cgrae19/cesA-19.
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/product= "Cellulose synthase"
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WPI; 2002-041338/05. P-PSDB; AAU10496.

New cellulose synthase polypeptides and polynucleotides, useful in improving stalk quality or silage, and in increasing concentration of cellulose in the pericarp, hardening the kernel for improved handling ability $\,$

Claim 4; Page 80-85; 88pp; English.

The invention relates to isolated nucleic acids encoding two cellulose synthase proteins from corn, ddpq45 (cesh-3) and cquealy (cesh-9).

Also disclosed are a recombinant expression cassette comprising the polynucleotide (operably linked to a promoter) a host cell comprising the recombinant expression cassette. The nucleic acid is useful in the recombinant expression cassette. The nucleic acid is useful in the improvement of stalk quality for improved stand or sliage, and in the improved and increased concentration of cellulose in the pericarp, hardening the kernel, and thus improving its handling ability. The nucleic acid supplies to be used as probes or amplification primers in the detection, quantification or isolation of gene transcripts, as probes in detecting deficiencies in the level of gene transcripts, as probes in detecting allelic variants, for monitoring up requiration of expression or clanges in enzyme activity in screening assays, for site directed mutagenesis, cell, tissue or plant. The polypeptides may be used in assays for enzyme agonists or antagonists, and as immunogen or antigen to contain antibodies specifically immunoreactive with the protein. The present sequence encodes a corn cellulose synthase of the

Sequence 3799 BP; 925 A; 931 C; 995 G; 944 T; 4 other;

; GACGICITCACCGCCTGCGACGICTGCCGCTTCCCGGTCTGCCGCCCCTGCTACGAGCAC 215 GGGAGCCCAGCGATCCGCGGGGGGGAGGCGACGACACTGATGCCGATGATGGTAGTGAC 335 AGCTGGCGCATGAACACCGGGGCCAGTGGCAATGTTGGCCACCCCAAGTATGACAGTGGC 455 GAGATCGGCCTCTCCAAGTATGACAGTGGAGAGATCCCTAGGGGGATACGTCCCTTCAGTC 515 CACGGGGCCGGGGACGTGTGCCAGATCTGCGCCGACGGCCTGGGCACCACGTTGGACGGC 155 TTCAACTACCCTGCATCTGGCACTGAGGACCAGAAGCAGAAGATTGCTGACAGGATGCGC 395 Gaps CGGGTTGGATCGCTCTGCCGCGCCATGGACGCGACGCGGACGCCCTGAAGTCCGGGAGG 95 4; DB 24; Length 3799; Score 2595; DB 24; Length Pred. No. 0; 0; Mismatches 420; Indels Query Match
Best Local Similarity 87.1%;
Matches 2871; Conservative 36 274 276 454 396 574 96 156 334 216 394 336 514 456 534 694 Q à à g δ g ò q ò qq à QQ ò qq à g

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V da	636	TCAAGGAGTTCTCCGGCAGTAI 	AATGTTGCCTGGAAAGAGAGTTGATGGCTGG 	695 873
δ	0 1	AAAATGAAGCAGACAAGGGTGG	ATGACTA	755
g à	756	PCGGGCAGCTACTG	TACTGAATACAACATGGAAGACGTTT	· -
qa	934		CATCAACTGATTACAACATGGAAGATGCCTTA	9
QY	816	SAATGAT	SAAAAGTCC	875
qq	994	SAAACTCGCCAGC	SACTICCTICCAGGAT	0
δλ	876	AATCCCTACAGAATGGTCATTGT	GGTTGGTTGTTCTAAGCATCTTCCTGCACTAC	935
qq	1054	CATACAGGATGGTCATT	rgattettetagcatettette	-
δ	936	CGTCTCACAAATCCTGTGCGTAA	CACTGTGGCTTTTAT	6
qq	1114	sgarcacaaarccrgrgcgr	acterecerrerarcrerrararerea	Н
Qy	966	ATTIGGTITGCTTTATCCTGGATA	AGTTCCCGAAGTGGT	105
qq	1174	creditrecrericies	TITCCAAAGIGGITICCAATCAACCG	123
δλ	1056	GAGACCTACCTTGATAGACTGGCT	ratgaccgagaaggtgaacc	1
qq	1234	raccrigaradacre	SACCEGGAAGETGAGCCATCTCAGTT	129
Oy	1116	GCTGCTGTTGACATATTTGTCAGT	SACCCCTTGAAGGAGCCACC	117
QQ	1294	CTGCTGTTGACATTTTTGTCAG	TCAC	e
δλ	1176	GCCAACACTGTGCTATCCATTCTT	PATC	~
qq	1354	ccaaraccerecrarccarrcr	TGTGGATAAGGTCTCTTGCTA	141
Qy	1236	GTATCTGATGACGGAGCTTCAATG	SACGCATTGGCTGAGAC	129
qq	1414	TGATGATGGAGCTGCTAT	GATGCACTAGCTGAGACTTCAGAGTT	4
δλ	1296	GCTAGGAAATGGGTACCATTTGTG	STATGACATTGAACCCAGAGCTCCCGAGTTT	3
QQ	1474	CTAGAAAATGGGTGCCATTTGT	CATTGAACCTAGAGCTCCTGAAT	
QY	1356	TACTITICCCAGAAAATIGATIACC	AGACAAAGTCCAGCCTTCATTTGTTAAAGAC	141
qq	1534	CTCCCAGAAATTGATT	CAAAGTGCACCCTTCATTTGTTAAAGA	S
δλ	1416	CGCCGGGCCATGAAGAGAGAATATG	ATTTAAAATCAGGATAAATGCCCTAGTTTCT	147
qo	1594	SCCGGCCATGAAGAGAGAATAT	CAAAATTAGGGTAAATGGCCTTGTTGC	9
QY	1476	AAGGCATTGAAAGTCCCCGAGGAAG	ATCATGCAAGATGGCACACCATGGCCAGGA	m
qq		SACAAAAGTCCCTGAG	CATGCAAGATGGCACACC	2
δλ	1536	AACAATACCAGGGATCATCCTGGAA	STTTTCCTTGGTCACAG	10
qq	1714	rccre	rtriccriggicacacigiggi	177
Qy	1596	GATACTGAGGGTAATGAGCTCCCCCC	PATGTGTCTCGTGAAAA	LO.
qq	1774	SAGGERATGAGETACC	ATGTTTCTCGTGAAAACGTCCT	183

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                                                       CTGATGGAATATGGTGGTGCTCCTCAGTCCTCCACACAGAATCTCTTTTGAAAGAAGCT
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unspecified amino acid"
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Wed Feb

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The present sequence encodes a maize cellulose synthase polypeptide.
The cellulose synthase can be used for the improvement of stalk quality for improved stand or silage. It also provides an increased concentration of cellulose in the pericarp, hardening the kernel and improving its handling ability. The sequences are used to produce transgenic plants and seeds expressing the cellulose synthase. The polymoclectide is and seeds expressing the cellulose synthase. The polymoclectide is as a probe or primer in the detection quantitation or isolation of gene transcripts. The probability of deficiencies in the level of mRNA in screenings for desired transgenic blant, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detecting mutations in the gene, for monitoring upregulation of expression or changes in plant breeding programs. The compounds, for detection of any number of allalic variants of the gene, cor for use as molecular markers in plant breeding programs. The recombinant expression of their encoded polypeptides or for use as immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antigonists of enzyme function or for use of immunogens or antigens to obtain
                                                                                                                       New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein -
     ×
     Wang
BA,
                                                                                                                                                                                                                          Claim 1; Page 137-141; 119pp; English.
  Bowen
Helentjaris TG,
                                                 2000-224343/19
                                                                      P-PSDB; AAY84114
Dhugga KS,
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Sequence 3746 BP; 861 A; 976 C; 1006 G; 902 T; 1 other;

ä 543 243 303 423 483 384 444 504 CCAGGCCCCAGGCTCCAGGCCAGCTCCCTCGACGTTTCTCGGCGAGCTCGCTTGCCATGG 324 Gaps 63 4 CGAGGAACCCCCCCTCCAGCTCTGTCGTCGGTGCGGGTTGGATCGCTCTGCCGCCCCATGG CCCAGTGCAAGACCAAGTACAAGCGCCACAAGGGGAGGCCCGGCGGCGATCCGTGGGGAGGAAG ACCAGAAGCAGAAGATTGCTGACAGGATGCGCAGCTGGCGCGTTGAACACCGGGGGCAGTG ACGCCGACGCGGACGCCCTGAAGTCCGGGGAGGCACGGGGCCGGGGACGTGTGCCAGATCT GCGCCGACGCCTGCGCACCACGTTGGACGGCGACGTCTTCACCGCCTGCGACGTCTGCC GCTTCCCGGTCTGCCGCCCCTGCTACGAGCACGAGGAGGAGGGCACCCAGGCCTGCC TCCAGTGCAAGACCAAGTACAAGCGCCACAGAGGGAGCCCAGCGATCCGCGGGGAAG GCGACGACACTGATGCCGATGATGGTAGTGACTTCAACTACCCTGCATCTGGCACTGAGG **ACCAGAAGCAGAAATTGCCGACAGAATGCGCAGCTGGCGCATGAACGTTGGGGGCAGCG** GCAATGTTGGCCACCCCAAGTATGACAGTGGCGAGATCGGCCTCTCCCAAGTATGACAGTG GAGAGATCCCTAGGGGATACGTCCCTTCAGTCACCAACAGCCAGATGTCAGGAGAAATCC Ouery Match 70.9%; Score 2572.2; DB 21; Length 3746; Best Local Similarity 86.4%; Pred. No. 0; Matches 2864; Conservative 1; Mismatches 439; Indels 9; 325 64 385 445 505 619 124 184 244 304 565 364 619 484 424 qq g 셤 8 g ò ò δ ò à ά g ö g ò 8

1158 843 963 GACCGCCGGCCATGAAGAGAATATGAAG CAGTCACTAACAGCCAGATCTCAGGAGAAATCC SCTGGAAAATGAAGCAGGACAAGGGTGCGATTC TGAGATTTGGTTTGCTTTATCCTGGATACTGG TGAGATCTGGTTTGCTCTTTCGTGGATATTGG CCGGGAGACCTACCTTGATAGACTGGCTTTAA GTTGGCTGCTGTTGACATATTTGTCAGTACAG CTATGTATCTGATGATGGAGCTGCGATGCTGA STITCCTAGGAAATGGGTACCATTTGTGAAGA ICTAAGGCATTGAAAGTCCCCGAGGAAGGAT ATCCGTCAAGGGAGTTCTCTGGTAGCATTGGGA CCTCTGAAGGTCGGGCAGCTACTGACATCGATG TITACTGAATGAAACTCGCCAGCCTCTAT CTTATTGAACGACGAAACTCGACAGCCTCTAT CTACCGTCTCACAAATCCTGTGCGTAATGCAT CACTGCCAACACTGTGCTATCCATTCTTGCTG CTATGTATCTGATGACGGAGCTTCAATGCTGA TTTGCTAGAAATGGGTACCATTTGTTAAGA STTTTACTTTGCCAGAAAATTGATTACCTGA GACCGCCGGCCATGAAGAGAGAATATGAAG GCTAAGGCACAGAAAGTTCCTGAGGAAGGAT CTTGATACTGAGGTAATGAGCTCCCCCGTT TGTCCCCTACGGGGAACATCAGCAGACGTGCTC **ITCCGTCAAGGGAGTTCTCCGGCAGTATTGGGA** GGAAACAATACCAGGGATCATCCTGGAATGA 1819 TTCAGGTTTTCCTTGGTCACAGTG AATTTAAAATCAGGATAAATGCC TTGATTATCCCGTGGACAAGGTC AATTCAAAGTTAGGGTAAATGGC TTCAGGTTTTCCTTGGTCACAGT 1459 TGGATTACCCTGTGGATAAGGTC AGGACAAGTGCACCCTTCATTT GGATCATGCAAGATGGCACACCA 1264 CTTTTGACGCATTGGCTGAGACT **AAGACAAAGICCAGCCIICAIII** GGATCATGCAAGATGGCACACCA 1144 TCGACCCCTTGAAGGAGCCACCT 1519 CATTTGATGCACTAGCTGAGACT AGTATGACATTGAACCCAGAGCT 1279 ATCAGTTCCCTAAGTGGTTTCC 1339 GGTATGACCGGGAAGGTGAGCC 1024 ATCAGTTCCCGAAGTGGTTTCC GGTATGACCGAGAAGGTGAACC 17111111111111 11 ATGTTGCCTGGAAAGAGAGGGT 979 CCATGACGAATGGCACAAGCAT 784 CATCTACTGAATACAACATGGA 844 CTAGAAAGTCCCCATTGCTTC 1099 CTAGGAAAGTTCCACTTCCTTC ACCCACTGTGGCTTTTATCTGT CGTTTCCCTATGTGAATCATTO ATGTTGCCTGGAAAGAGAGAGT 724 CCATGACTAATGGGACAAGCAT 1039 CATCAACTGATTACAACATGGA GGTTGGTTGTTCTAAGCATCTT 219 ACCCATTATGGCTTCTATCTGT 799 CTGGTGCTTCCCCTGACCATCA 1159 GATTGATTGTTCTAAGCATCTI CTGGAGCTTCGCCTGATCATCI 739 GCGAGATICCICGGGGATACA 859 CATTICCCTATGTGAACCATT 544 664 919 964 1084 1204 1579 1384 1639 6691 1504 1564 604 904 1324 1444 ογ g ŏ q δy q δ QΩ δ g Qγ ద Q Dp QΛ g S B S qq O Dp oγ Q ά q ò g Ôχ g οy a à Q οŽ

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     TGGTCTATGTTTCTCGTGAAAAGCGTCCTGGATTCCAGCATCAAAAGGTGGTGCCA
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TCATCATGCCAGAGATTAGCAACTTGGCCAGTATCTGGTTCATTGCGCTCTTCCTTTCAA
        GGAATGAACAGTTCTGGGTCATTGGAGGTATCTCTGCACATCTGTTTGCCGTCTTTCAGG
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transgenic plant; plant breeding
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The present sequence encodes a maize cellulose synthase polypeptide.
The cellulose synthase can be used for the improvement of stalk quality
for improved stand or silage. It also provides an increased concentration
of cellulose that he pericarp, hardening the kernel and improving its
handling ability. The sequences are used to produce transgenic plants
and seeds expressing the cellulose synthase. The polynucleotide is
used for modulating, preferably increasing, the level of the synthase
in a plant cell. The plants are preferably monocots. The polynucleotide is
solation of gene transcripts. The probes are useful in detecting
deficiencies in the level of mRNA in screening for desired transgenic
plant, for detecting mutations in the gene, for monitoring upregulation
compounds, for detecting mutations in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection any number of allelic variants of the gene,
or for use as molecular markers in plant breeding programs. The
combinant expression of their encoded polypeptides or for use as
immunogens in the preparation and/or screening of antibodies. The
crecombinant expression of their encoded polypeptides or for use as
immunogens in the preparation and/or screening of antibodies. The
crecombinant expression or for use of immunogens or antigens to obtain
continued to the compounds of antibodies or contains to obtain
contains an employed in assays for enzyme agonists or obtain
                                                                                                                                                                                                                                                    New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein -
                                                                                                                               Wang X;
                                                                                                                               Bowen BA,
                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 176-181; 119pp; English.
                                                                           (PION-) PIONEER HI-BRED INT INC.
                      98US-0096822.
                                                                                                                          Dhugga KS, Helentjaris TG,
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P-PSDB; AAY84119.
                      17-AUG-1998;
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Sequence 3746 BP; 861 A; 976 C; 1006 G; 902 T; 1 other;

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tch	Best Local Similarity 86.4 Matches 2864; Conservative	CGAGGAACCC	CCAGGCCCCAC	ACGGCGACGC		GCGCCGACGGC				TCCAGTGCAAC	CCCAGTGCAAC	GCGACGACACT	GAGACGACACT		ACCAGAAGCAC	GCAATGTTGG	
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a- a	SCIATGTATCTGATGACGGAGCTTCAATGCT 	SATTATCCGTGGACAAGGT
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8 - 8 - 1	AAATAATCCCTACAGAATGGTCATTGTTCTGC	CTAGAAAAGTCCCCATTGCTTC
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                                                                GGAATGAACAGTTCTGGGTCATTGGAGGTATCTCTGCACATCTGTTTGCCGTCTTTCAGG
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an
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/product= "cellulose synthase"
/transl_except= (pos: 1817..1819, aa: Xaa)
/note= "no termination codon given; Xaa is
unspecified amino acid"
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transgenic plant; plant breeding
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The present sequence encodes a maize cellulose synthase polypeptide.
The cellulose synthase can be used for the improvement of stalk quality
for improved stand or silage. It also provides an increased concentration
of cellulose in the pericarp, hardening the kernel and improving its
handling ability. The sequences are used to produce transgenic plants
and seeds expressing the cellulose synthase. The polynucleotide is
used for modulating, preferably increasing, the level of the synthase
in a plant cell. The plants are preferably monocots. The polynucleotide is
stato used as a probe or primer in the detection quantitation or
isolation of gene transcripts. The probes are useful in detecting
deficiencies in the level of mRNA in screenings for desired transgenic
plant, for detecting mutations in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection of any number of allelic variants of the gene,
or for use as molecular markers in plant breeding programs. The
                                                                                                                                                                                                                                                                                                                                                            New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or for use as molecular markers in plant breeding programs. The isolated nucleic acids of the present invention can also be used for recombinant expression of their encoded polypeptides or for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3773 BP; 863 A; 988 C; 1017 G; 904 T; 1 other;
                                                                                                                                                                                                                                            Wang X;
                                                                                                                                                                                                                                            Bowen BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 90-94; 119pp; English.
                                                                                                                                                                                            PION-) PIONEER HI-BRED INT INC.
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P-PSDB; AAY84108.
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5 GCTTCCGGTCTGCCGCCCCTGCTACGAGCACGCAAGGAGGGCACCCAGGCCTGCC 243 363 64 ACGCCGACGCGCACGCCCTGAAGTCCGGCACGCGCCCGGGGACGTGTGCCAGATCT 123 124 GCGCCGACGGCCTGGGCACCACGTTGGACGGCGACGTCTTCACCGCCTGCGACGTCTGCC 183 244 TCCAGTGCAAGACCAAGTACAAGCGCCACAGGGAGCCCAGCGATCCGCGGGGGAGGAAG 303 522 CCCAGTGCAAGACCAAGTACAAGGCCCACAAGGGGAGCCCGGCGGTCCGTGGGGAGGAAG 581 9; Gaps 4 CGAGGAACCCCGCTCCCAGCTCTGTCGTCGGTGCGGGTTGGATCGCTCTGCCGCGCCATGG 63 462 GGTTTCCGGTGTGCCGCCCCTGCTACGAGTACGAGCGCAAGGACGGCACGCAGGCGTGCC GCGACGACACTGATGCCGATGATGGTAGTGACTTCAACTACCCTGCATCTGGCACTGAGG Score 2572.2; DB 21; Length 3773; Pred. No. 0; 439; Indels 1; Mismatches 70.98; 86.48; Query Match 70.9 Best Local Similarity 86.4 Matches 2864; Conservative 184 304 582 g QQ q g Db ò ò ò οŽ ò δ

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ΟΥ Db	Qy Db	oy Op	ò a	Q	oy Db	oy Og	Oy Dp	Oy Dp	Qy Dp	oy Ob	Qy Db	oy Ob	δ q	oy Db	o d	QY Db	QY Db	δλ

Db 2793 GGGCTCTTGGGTCGTGGAGATCTCTTCAGCCGGCACTGCCCCCTGTGGTACGGCTACG 2852	Db 2973 TCATCATCCAGGAACTTCGCCAGCATCTGGTTCATCTCCTCTTTTTTTT	3093 GGAACGAGCAGTTCTGGGTGATCGGGGCATCTCGCGCACCTCTTCGCCGTGTTCCAGG 2884 GTCTTCTGAAGGTGCTTGCGGTATCGACCAACTTCACTGTCACTCAAGGCTAATG 1	QY 2944 ACGAGGGGACTTTGCTGAGCTCTACATGTTCAAGTGGACGTCTCATCATCTCTC 3003	3273	318	3453	ACCCTTCACCACCGGGTCACTGGCCGGGTACCCAGACGTGGGCATCAACTGCTAGG AAAGTGGGGATTT 3316	RESULT 5 AA299533 ID AA299533 standard; DNA; 3704 BP.	XX AA299533; XX DT 03-JUL-2000 (first entry)	DNA en Maize;	cation/Qualifiers	
	Oy 1624 IACTTANGREGEGGEGAAAGGGGGGGGGGGGGGGGGGGGGGGGGG	1744 ATTGTGATCACTACAACAACAGGGAGGCTGTCCGAGAACCTATGTGCTTCCTAATGG 180 1111111111111111111111111111111111	20/0 AUCTANCCIAGGAAGGAGGTCIGCIACGICCCAGGAGAIICGAIGGCATIG 213 1864 ATAGGAATGATCGATATGCAAACAGGAACACTGTCTTTTTTGATATTAACTTGAGGGGCC 192 2136 ACAGGAATGATGGATATGCCAACAGGAACACGTGTTTTTGATATTAACTTGAGAGGTC 219	1924 TYGACGCATTCAAGGACCACTTAYGTGGGAACTGGTTGTGTTTCAACAGAACAG	DD 2256 TATATGGTTATGAGCCCCCAATTAAGCAGAAGGGTGGTTTCTTGTCATCACTATGTG 2315 Qy 2044 GGGGAAGAAGAGCAAGCAAGTCAAAGAAAGGAGCTCAGATAAGAAAAGGGAACA 2103 DD 2316 GCGTTAGGAAGGCAAGCCAAATCAAAGAAAGGGTCGGAAAAAAAGTCGCAAGAAAGGCAAAGAAAGCCAAAAAGCAAAAAGAAAGGGTCGGAAAAAGAAAGGCAAAAAAAAAA	2104 AGCATGGACAGTTCTGTTCCAGTATTCAATCTCGAAGACATAGAGGAGGGTGTTGAAG 11111111111111111111	Qy 2164 GTGCTGGGTTTGATGAGAAATCAGTTCTCATGTCTCAAATGAGCTTAGAGAGAT 2223 Db 2433 GCGTGGATTTGACGACGAGAAATCACTTCTTATGTCTCAAATGAGCTGGAGAAGAGT 2492 Qy 2224 TTGGCCAGTCAGCACTTTGTTGCTCCACTCTGAATATGGTGTTCTCAGT 2283 Qy 111111111111111111111111111111111111	2284 CCTCCACTCCGGAATCTCTTTCGAAAGCTATCCATGTCATGTGGCTATGAGGCTATGCGTATGTGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGCTATGAGGGCTATGAGGGCTATGAGGGCTATGAGGGCTATGAGGGCTATGAGGGCTATGAGG	Qy 2344 ACAAGTCTGAATGGGGAACTGAGATTGGTTGGATCTGTGACTGTCACAGAAGATATTC 2403 	Qy 2404 TTACTGGATTCAAGATGCACGCAAGAGGCTGCGGTTCAGTCTATTGCATGCCCAAGCGC 2463 I <td< td=""><td>Oy 2464 CAGCTTTCAAGGGATCTGCCCCATCAACTTTCAGATCGTCTGAACCAAGTGCTGGGT 2523 </td><td></td></td<>	Oy 2464 CAGCTTTCAAGGGATCTGCCCCATCAACTTTCAGATCGTCTGAACCAAGTGCTGGGT 2523	

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The present sequence encodes a maize cellulose synthase polypeptide.

The cellulose synthase can be used for the improvement of stalk quality
for improved stand or silage. It also provides an increased concentration
of cellulose in the pericarp, hardening the kernel and improving its
handling ability. The sequences are used to produce transgenic plants
and seeds expressing the cellulose synthase. The polymucleotide is
used for modulating, preferably increasing, the level of the synthase
in a plant cell. The plants are preferably monocots. The polymucleotide
is used for modulating, preferably moreasing, the level of the synthase
constant cell. The plants are preferably monocots. The polymucleotide
is also used as a probe or primer in the detection quantitation or
isolation of gene transcripts. The probes are useful in detecting
deficiencies in the level of mRNA in screenings for desired transgenic
compounds, for detections in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection of any number of allelic variants of the gene,
corporated acids of the present invention can also be used for
recombinant expression of their encoded polypeptides or for use as
immunogens in the preparation and/or screening of antibodies. The
proteins can be employed in assays for enzyme agonists or obtain
constant and any and any or enzyme aponists or antagonists
and antibodies specifically immunoreactive with a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein
                                                    an
/product- "cellulose synthase"
/transl_except- (pos: 1544..1546, aa: Xaa)
/note- "no termination codon given; Xaa is
unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3704 BP; 909 A; 838 C; 962 G; 994 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                      Wang X;
                                                                                                                                                                                                                                                                                                                                                      Bowen BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 191-196; 119pp; English.
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P-PSDB; AAY84121.
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4 98 CGGGGCCGGGGACGIGIGCCAGAICIGCGCCGACGGCCIGGGCACCACGIIGGACGGCGA 157 CGTCTTCACCGCCTGCGACGTCTGCCGCTTCCCGGTCTGCCGCCCTGCTACGAGCACGA 217 277 GAGCCCAGCGATCCGCGGGGGAGGCGACGACGACTGATGCCGATGGTAGTGACTT 337 12; Gaps 38 GGTTGGATCGCTCTGCCGCGCCATGGACGGCGACGCGGACGCCCTGAAGTCCGGGAGGCA 97 GCGCAAGGAGGGCACCCAGGCCTGCCTCCAGTGCAAGACCAAGGTACAAGCGCCCACAGAGG DB 21; Length 3704; 549; Indels 64.1%; Score 2325.2; 82.8%; Pred. No. 0; iive 0; Mismatches Best Local Similarity 82.8 Matches 2706; Conservative Query Match 158 487 218 278 427 à 원 à g ö q g ò à

TCTGGG 1-1-1-1 1-1-1 1-1-1 1-1-1 1-1-1 1-1-1 1-1-1 1-1-1 1-1-1 1-1-1 1-1-1 1-1-1 1-1 1-1-1 1	AACACACCTGCATCTGGCACT [111] 111] 111] 111] ATTGGCGACAACTCAGGGAGA TGGCGGACAACTCAGGGAGA ATGGCCATGGAAGTATCAGGAGA [11] 11] 11] 11] 11] ATTGGCCATGGAAGTATCAGGAGA ACGGGAACATCAGGAGAGA AGGGAACATCAGGAGAGA AGGGAACATCAGGAGAGA AGGGAACATCAGGAGAGA AGGGAACATCAGCAGAGA AGGGAACATCAGCAGAGA AGGGAACATCAGCAGACATCAGAGAGA AGGGAACATCAGCAGCATCATCAGAGAGAGAGAGAGAGAG	338 CAACTACCCTGCATCGGCACT 547 CAACTACCAGGCACT 547 CAACTACCAGGCACT 607 TTGGCGGACATCACCAGGCG 458 GATCGCCTCTCCAGTAGC 518 CAACTGCGGACATCACGGGGAA 724 TAGGCGGACATCACGGGAA 724 TAGGCGGACATCACGGGAGGA 578 TACGGGGACATCACGGGAGGA 578 TAGGCACATCCCGGCAGTATC 1 1 1 1 1 1 1 1 1 1
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2698	2758	Qy 2618 CAT Db 2818 TAT	Qy 2678 TGC 1 Db 2878 AGC	Qy 2738 CTG Db 2938 TTC	QY 2798 TGC Db 2998 TGC	285	DD 3058 TGC	3118	Qy 2978 CAJ Db 3178 CAJ	3038	Db 3238 GG		Qy 3158 GG		Qy 3218 CT 	3278	3478	3UL		AC AAZ5827 XX DT 08-MAY-	XX DE Wheat C XX		Key	FT CDS
1418 CCGGGCCATGAAGAGAATATGAAGAATTTAAAATCAGGATAAATGCCCTAGTTTCTAA 1477 	1478 GGCATTGAAAGTCCCCGAGGAAGGATGGATCATGCAAGATGGCACACCATGGCCAGGAAA 1537 		TACTGAGGGTAATGAGCTCCCCGTTTAGTTTATGTGTCTCGTGAAAAGCGTCCTGGGTT 16	CGTTGARGGCARTGARCTICCTCGTTTTGTGTTTATGTGTCTCGTGARARACGTCTGGGGTTTTGTGTGTTCGTGTTCGTGTTCGTGTTCTTAC 171		1921 TAATGGGCAATACATGTTGAATCTTGATGGTGACCACTACATCAATAATAGGAAGGGTCT 1980 1778 CCGAGAAGGTATGTGCTTCCTAATGGATCCAAACCTAGGTCCGCAAGTCTGTTATGTGCA 1837		1838 GTICCCACAAAGGTITGAIGGGAITGAIAGGAAIGATCCAIAIGCAAACAGGAACACIGI 1897 	CTTTTTGATATTAACTTGAGGGCCTTGACGGCATTCAAGGACCAGTTTATGTGGGAAC	2101 GTTTTTCGATATTAACTTGAGGGTCTTGACGGCATTCAAGGGCCAGTTTATGTGGGAAC 2160 1958 TGGTTGTGTTTTCAACAGAACAGCTATGTATGGTTATGAGCCCCCAATTAAGGGGAAGAA 2017	TGGTTGTGTGTTTAACAGAACGCCCTTATATGGTTATGAGCCCCCAGTCAAGAAAAA	GCCAGGTTTCTTGGCATCACTATGTGGGGCAAGAAGAAGGCAAGCAA		2078 GAGCTCAGATAAGAAAAGTCGAACAAGCATGTGGACAGTTCTGTTCCAGTATTCAATCT 2137 2078 GAGCTCGGAAAGAAGAAGAAGACAGCAGAACATTCTGTACCAGTATTAATCT 2137 2278 GAGCTCGGAAAGAAGAAGAAGAACAATAACAAGAAGAAGAAAATACTAATTAAT		2338 CGAAGATATAGAGGAAGGGATTGAAGGTTCTCAGTTTGATGATGAGAATCGCTGATTAT 2397	2198 GICICAAATGAGCTIAGAGAAGAATIIGGCCAGTCAGCAGCATIIGIIGCCTCCACICI 2257 	B GATGGAATATGGTGGTGGTTCCTCAGTCCTCCAGAATCTCTTTTGAAGAAGCTAT	B GAIGGAAIAIGGIGGIGTICCACAAICIGCAACICCAGAGICICTICIGAAAGAAGCIAI 2	2318 CCATGTCATAAGTTGTGGCTATGAGGACAAGTCTGAATGGGAACTGAGATTGGTTGG	8 CTATGGATCTGTCACAGAAGATATTCTTACTGGATTCAAGATGCACGCAAGAGGCTGGCG 2	B CIAIGGIICIGITACAGAAGACAITCICACCGGAITCAAGAIGCAIGCICGGCG	2438 TYCAGITATICALATUCCCAAGCCTTTCAAGGATTTGCCCCATCCAATCTTTC 2*57 2638 ATCAATCTACTGCATGCCTAAGCGACCAGCTTTCAAGGATCTGCTCCTATCAACCTTTC 2697	2498 AGAICGICIGAACCAAGIGCIGCGGIGGGCICTCGGITCIGITGAAAITCITITCAGCCG 2557
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                                                                                                                                                                                                                                                                              The present sequence is that of a contig of cDNA clones and encodes a portion (see AAYS8840) of wheat cellulose synthase (CS). The cDNA clones were isolated from wheat 7-day seedling leaf and 7-day etiolated seedling root tissue cDNA libraries on the basis of cetiolated seedling root tissue cDNA libraries on the basis of homology to Arabidopsis and cotton CS sequences. The invention relates to isolated nucleic acid fragments encoding plant CS and to CS polypeptides. It also relates to the construction of a chimeric gene encoding all or a portion of the CS, in sense or antisense orientation, where expression of the gene results in altered levels of the CS in transformed host cells. The host cells can be used to screen compounds for their ability to inhibit CS activity. CS nucleic acids are also useful for producing transgenic plants having altered levels of CS, and hence altered levels of fibre. CS may also serve as a target for the development of novel herbicides.
                                                                                                                                                                                                             Nucleic acid fragments encoding cellulose biosynthetic enzyme useful as probes for isolating cDNAs and genes encoding homologous proteins, for producing transgenic plants
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Pred. No. 0;
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P-PSDB; AAY58840.
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2681 2441 2621 2801 2861 FGFCFGGGCFGCCFCCTCGCTTCTATCTTC 1441 GGAGTTTGTAGAGACAGAAATATAACAGTGA 3341 SAAGGCGACTTTGCTGAGCTCTACATGTTCAAG 1201 781 961 CTCCAGAATCTCTTTGAAAGAAGCTATCCAT CAGTCAGCAGCATTTGTTGCCTCCACTCTGATG CTGAATGGGGAACTGAGATTGGTTGGATCTAT GGATTCAAGATGCACGCAAGAGGCTGGCGTTCA GTTACCAATCATGGGGGCCGCTCTTTGGGAAG SGATTCAAGATGCACGCAAGAGGCTGGCGTTCA TCAAGGGATCTGCCCCCATCAATCTTCAGAT STCGGTTCTGTTGAAATTCTTTTCAGCCGGCAT CCCCTCAAGTTCCTGGAGAGATTCGCTTACATC CGCCTCAAGTTCCTGGAGAGATTCGCTTACATC TCCCGCTTCTAGTCTATTGTATTGCCTGCT TCCCGCTTCTAGTCTATTGTATATTGCCTGCT TGCCAGAGATTAGCAACTTGGCCAGTATCTGG CCACTGGTATCCTTGAGATGAGGTGGAGTGGT SCCACTGGTATCCTTGAGATGAGGTGGAGTGGT AACAGITCTGGGTCATTGGAGGTATCTCTGCA GAAGGTGCTTGCCGGTATCGACACCAACTTC **AAGGCGACTTTGCTGAGCTCTACATGTTCAAG** CCATTTTGATCATTAACATGGTTGGTGTCGTT GTTACCAATCATGGGGGCCGCTCTTTGGGAAG ACTIATACCCATTCCTCAAGGGTCTTATGGGC **FCACTACCCGTCTCGCTGGCCCAAATATCCAA** TCGTCTGGGCTGTCCTCCTCGCTTCTATCTTC ACTGTCACCTCAAAGGCTAATG TGGACGACGCTTCTCATCCCTC GCTGGCACCTCCTACGCCATCA GCTGGTACCTCCTACGCCATCA CTCTTCTTTGCCTTCTGGGTGA CTCTTCTTGCCTTCTGGGTGA 1382 AGGCAAAACCGCACACCGACGA TCCTTGCTGTGGGTTCGTGTTG 3282 ACCTGTGGCATCAACTGCTAGG TTCATTGCGCTCTTCCTTTCAA 962 ITCATIGCGCTCTTCCTTTCAA GTTGGCATTGACGAGTGGTGGA CATCTGTTTGCCGTCTTTCAGG ACTGTCACCTCAAAGGCTAATG AGGCAAAACCGCACACGACGA TGCCCCTTATGGTATGGCTACG 782 TGCCCCTTATGGTATGGCTACG 2682 ATCTGTCTGCTCACTGGAAAGT GTTGGCATTGACGAGTGGTGGA CATCTGTTTGCCGTCTTTCAGG TGGACGACGCTTCTTATCCCTC CGTCTGAACCAAGTGCTGCGGT CGTCTGAATCAAGTGCTGCGGT CAAATGAGCTTAGAGAAGAGAI CAAATGAGCTTAGAGAAGAGAT GAATATGGTGGTGTTCCTCAG GAATATGGTGGTGTTCCTCAG GTCATAAGTTGTGGCTATGAGG GTCATAAGTTGTGGCTATGAGG GGATCTGTCACAGAAGATATTC GGATCTGTCACAGAAGATATTC GTCTATTGCATGCCCAAGCGCC

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       3461
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                                                                                             Hybridisation assay, genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                   Arabidopsis thaliana DNA fragment SEQ ID NO: 61572.
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Library using probes obtained by PCR with primers (see AAT99632-34)

Library using probes obtained by PCR with primers (see AAT99632-34)

Eased on cellulose synthase RSM1 genomic clone 13H12 (see AAV06563)

and encodes a 1065-pollypeptide (see AAW3819). Claimed nucleic acid
and encodes a 1065-pollypeptide (see AAW3819). Claimed nucleic acid
molecules (see AAV06562-69) coding for claimed pollypeptides (see AAW3816-20) and AAW46202) involved in cellulose biosynthesis can be
used to manipulate the cellulose and/or beta-glucan content of
transgenic plants. Expression of nucleic acids in the sense
crientation increases the level of cellulose and reduces the level
of non-crystalline beta-1.4-glucan and starch, providing plants
with modified strength and/or shape and/or fibre properties, or
having increased resistance to stresses or pests. Antisense,
closuppression molecules can be used to reduce the
cellulose content of a transgenic plant, e.g. to improve
digestibility or to alter carbon partitioning such that increased
carbon is available for growth, rather than deposited as cellulose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding cellulose biosynthetic enzyme - useful for manipulation of cellulose and beta-1,4-glucan
                                                                                                                                                               Cellulose; cellulose synthase; RSW1 gene; beta-1,4-glucan; transgenic plant; ss.
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                                                                                                                                Arabidopsis cellulose biosynthetic gene clone Ath-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williamson RE;
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                                AAV06567 standard; cDNA; 3614 BP.
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                                                              AAV06567;
RESULT 8
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ώ ώ Score 1673.6; DB 19; Length 3614; Pred. No. 0; 0; Mismatches 869; Indels 72; Gaps 30 TCGGTGCGGGTTGGATCGCTCTGCCGCGCCATGGACGCGACGCGGACGCCCTGAAGTCC 89 Query Match Best Local Similarity 71.4% Matches 2347; Conservative ŏ Q

46.28; 71.48;

90 GGGAGGCACGGGGCCGGGACGTGTGCCAAATCTGCGCCGACGACCAGGTTG 149

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oy d	150	GACGGGACGTCTTCACCGCCT	SGTCTGCCGCTTCCCGGTCTGCCGCCCCTGCTAC 209
3 8	310		2
2 2	370	GAGCACGAGCGCAAGGAGGGCA 	SUCCITECTICLAGISCAAGACCAAGIACAAGIACAAGIAC 289
Qy	270		32
qq	430	CTCAAAGGTAGTCCTGCTATTC	
οy	330		GGCACTGAGGACCAGAAGCAGAATTGCTGAC 386
QΩ	490	ACTGTTGAGTTCAACTACCCT-	
Oy	387	AGGATGCGCAGCTGGCGCATGA	GGGGGCAGTGCATGCCACCCCAAGTAT 446
Op	532		GGGAAGGGAATGGGGGAACCCCAGTAT 591
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Qy	567	ATGATGTCCCCTACGGGGAACA	AGACGTGCTCCGTTTCCCTATGTGAATCAT 623
Op	682		AAGGGCTTCCCTATTCATCAGATGTAA 741
Oy	624	TCACCAAATCCGTCAAGGGAGT	GGCAGTATTGGGAATGTTGCCTGGAAAGAGAGA 683
Dp	742	TCACCAAATAGAAGGATTGTGG	GTTGGACTCGGGAATGTAGCTTGGAAGGAGAGA 801
Qy	684	GTTGATGGCTGGAAAATGAAGC	AAGGGTGCGATTCCCATGACTAATGGGACAAGC 743
Ор	802		AAGAATACTGGTCCTGTCAGCACG 852
δλ	744	ATTGCTCCCTCTGAAGGTCGGG	ACTGACATCGATGCATCTGAATACAACATG 803
QQ	853	CAGGCTGCTTCTGAAGAGGTG	TAGATATTGATGCCAGCACAGATATCCTAGCA 909
QY	804	GAAGACGCTTTACTGAATGATG	GGCCAGCCTCTATCTAGAAAAGTCCCCATTGCT 863
Op	910		AGGCAGCTTCTGTCAAGGAAAGTTTCAATTCCT 969
Qy	864	TCCTCCAAATAAATCCCTACA	STCATIGITCIGCGGIIGGIIGTICIAAGCAIC 923
qq	970		20
δλ	924	TICCIGCACTACCGICICACAA	SIGCGTAATGCATACCCACTGTGGCTITIAICT 983
g	1030		108
δλ	984	GTTATATGTGAGATTTGGTTTGC	CCTGGATACTGGATCAGTTCCCGAAGTGGTTT 1043
qq	1090	GIGATATCTGAGATCTGGTTTGC	CCTGGATTTGGATCAGTTTCCCAAGTGGTTT 1149
ογ	4	CCAATCAACGGGAGACCTACCT	AGACTGGCTTTAAGGTATGACCGAGAAGGTGAA 1103
QQ	1150	CCTGTGAACCGTGAAACCTACCT	120
δλ S	10	CCGTCTCAGTTGGCTGCTGA	16
2	1210	CCATCACAGITAGCTGCTGTTGA	176
ζζ G	1164	CCTATCGTCACTGCCAACACTGT	CCATTCTTGCTGTTGATTATCCCGTGGACAAG 1223 CTATTCTGGCTGTTGACTACCCAGTTGACAAG 1329

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GTCTTGCTATGTATCTGATGACGGAGCTTCAATGCTGACTTTGACGCATTGGCTGAG	GCCCTAGTTTCTAAGGCATTGAAAGTCCCCGAGGAAGGATGGAT	AATGGTGGACTTGATGCAGGGCAATGAGCTCCCGCGTTTGGTATATGTTTTCTCGAAAGGCTCCCGCGTTTTGGTATATGTTTTCTCGAAAGGCTGGTGCCATGAATTGCTTGTTTTCTGTTTTTTTT	AACAGCAAGGCTGTCCGAGAAGCTATGTGCTTCCTAATGGATCCAAACCTAGGTCC			GATGAGAAATCAGTTCTCAAATGAGCTTAGAGAAGAGATTGGCCAGTCAGCA
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3017 3197 2889 2837 2949 2897 2957 3069 3077 3249 2590 TCTGCTCCTATCAATCTTTCAGATCGTCTGAACCAAGTGCTGAGGTGGGCTTTAGGTTCA 2649 2597 2657 2717 2777 2950 IGGGTCATTGGTGGAGTATCCGCTCATTTATTCGCTGTGTTTCAAGGTATCCTCAAAGTC 3009 ATGCACGCAAGAGGCTGGCGTTCAGTCTATTGCATGCCCAAGCGCCCAGCTTTCAAGGGA 2477 CTTGCCGGTATTGACACAAACTTCACAGTTACCTCAAAAGCTTCAGATGAAGACGAGAC ATCCTTGAGATGAGGTGGAGTGGTGTTGGCATTGACGAGTGGTGGAGGAATGAACAGTTC TGGGTCATTGGAGGTATCTCTCCACATCTGTTTGCCGTCTTTCAGGGTCTTCTGAAGGTG TTTGCTGAGCTCTACATGTTCAAGTGGACGACGCTTCTCATCCTCCGACGACCATTTTG ATCATTAACATGGTTGGTGTTGTTGCTGCTGCTCCTACGCCATCAACAGTGGTTACCAA CCATTCCTCAAGGGTCTTATGGGCAGGCAAAACCGCACACCGACGATTGTCATCGTCTGG GTTGAAATTCTTTTCAGCCGGCATTGCCCCTTATGGTATGGCTACGGAGGGCCCCTCAAG ATTAGCAACTTGGCCAGTATCTGGTTCATTGCGCTCTTCCTTTCAATTTTCGCCACTGGT CTTGCCGGTATCGACACCAACTTCACTGTCACCTCAAAGGCTAATGACGAAGAAGGCGAC TCATGGGGGCCGCTCTTTGGGAAGCTCTTCTTTGCCTTCTGGGTGATTGTTCACTTATAC TCTCTTTTGAAAGAAGCTATCCATGTCATAAGTTGTGGCTATGAGGACAAGTCTGAATGG GGAACTGAGATTGGTTGGATCTATGGATCTGTCACAGAAGATATTCTTACTGGATTCAAG CTAGTCTATTGTATATTGCCTGCTATCTGTCTGCTCACTGGAAAGTTCATGCCAGAG TCTGCCCCCATCAATCTTTCAGATCGTCTGAACCAAGTGCTGCGGTGGGCTCTCGGTTCT 3417 CGTCTCGCTGGCCCAAATATCCAAACCTGTGGCATCAACTGCTAGGAA 3305 2710 2770 2718 2830 2890 2838 3010 3018 2778 2898 2958 3070 3130 3078 3250 3370 2418 3138 2530 2478 2650 2598 2658 2298 2470 2538 q Dp g Q D g 0y 0b oy Oy 90 90 90 90 90 07 07 08 δ Ω ò QΥ Ω Oy Oy

RESULT 9 AAZ99500 ID AAZ99500 standard; DNA; 3725 XX

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CCTTGCTATGAGTACGAGCGCAAGGAAGGAA 417

TACAAGCGCCACAGAGGGAGCCCAGCGATCCG

GATGATGGTAGTGACTTCAACTACCCTGCATC

GACCTGGACAATGAATTCAACTATAAGCAAGG

CCCTGCTACGAGCACGAGGCGCAC

Page 18

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 ATGACCCACACCATCGGATTCCACGCCTTACA

TACGTCCCTTCAGTCACCAGAGGCCAGATGTC

AAGTATGACAGTGGCGAGATCGGCCTCTCCAA

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1070 TAGACTGGCTTTAAGGTATGACCG
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                 173 CGACGTCTGCCGCTTCCCGGTC
                                             358 CAATGAGIGIGCCITCCCIGIC
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The cellulose synthase can be used for the improvement of stark quality
for improved stand or silage. It also provides an increased concentration
of cellulose in the pericarp, hardening the kernel and improving its
handling ability. The sequences are used to produce transgenic plants
and seeds expressing the cellulose synthase. The polynucleotide is
used for modulating, preferably increasing, the level of the synthase
of in a plant cell. The plants are primer in the detection quantitation or
isolation of gene transcripts. The probes are useful in detecting
deficiencies in the level of mink in screening for desired transgenic
CC plant, for detecting mutations in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection of any number of allelic variants of the gene,
or for use as molecular markers in plant breeding programs. The
confounds caids of the present invention can also be used for
recombinant expression of their encoded polypeptides or for use as
immunogens in the preparation and/or screening of antibodies. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 GTGCCAGATCTGCGCCGACGGCCTGGGCACCACGTTGGACGGCGACGTCTTCACCGCCTG 172
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                                                                                     Maize; cellulose synthase; stalk quality; stand; silage; cellulose; transgenic plant; plant breeding marker; ss.
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179.3398
/*tash
/*roduct= "cellulose synthase"
/note= "no termination codon given"
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                                                        DNA encoding a maize cellulose synthase.
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66.8%;
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Matches 2147;
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771

CATTCACCAAATCCGTCAAGGGAGTT---CTC

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TTTCCTCAAACCAGCTCAACCTTTACCGGAT

TTGCTTCCTCCAAATAAATCCCTACAGAAT

SCATCTTCCTGCACTACCGTCTCACAAATCC

TATCTGTTATGTGAGATTTGGTTTGCTTT

ACAAGGTCTCTTGCTATGTATCTGATGACGG

AACCTCCACTGATCACAGCCAACACTGTTTT 1290

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AGCTTCAATGCTGACTTTTGACGCATTGGCTGAGACTTCAGAGTTTGCTAGGAAATGGGT	ACCATTIGIGAAGAAGIATGACATIGAACCCAGAGCTCCCGAGTTTTACTITIGCCAGAA 	aatigattaccigaaagacaaagtccagcciicattigitaaagaccgccggccaigaa 	GAGAGAATATGAAGAATTTAAAATCAGGATAAATGCCCTAGTTTCTAAGGCATTGAAAGT 	CCCCGAGGAAGGATGGATCATGCAAGATGGCACCATGGCCAGGAAACAATACCAGGA 	TCATCCTGGAATGATTCAGGTTTTCCTTGGTCACAGTGGTGGCCTTGATACTGAGGGTAA 	tgagctccccctttagtttatgtgtctcgtgaaagcgtcctgggttccagcaccacaa 	GAAGGCTGGTGCCATGAATGCCCTTGTTCGTGTCTCAGCTGTCCTTACTAATGGACAATA	CATGITGAATCITGAITGIGAFCACTACAACAACAACAAGGCIGICCGAGAAGCIAT 	GFGCTTCCTAATGGATCCAAACCTAGGTCGGAAGTCTGTTATGTGCAGTTCCCACAAG 	GTTTGATGGGATTGATAGGAATGATGGATATGCAAACAGGAACACTGTCTTTTTGATAT 	TAACTIGAGGGCCTIGACGGCAITCAAGGACCAGITIAIGIGGGAACIGGITGIGITIT 	CAACAGAACAGCTATCTATGGTTATGAGCCCCCAATTAAGGCGAAGAGCCAGGTTT 	cttgccatcactatgtgggggaagaagaaggcaagcaagtcaaagaaag	TAAGAAAAAGTCGAACGAGCATGTGGACAGTTCTGTTCCAGTATTCAATCTCGAAGACAT 	AGAGGAGGGTGTTGAGGTTTGATGAGAAATCAGTTCTCATGTCTCAAAT	GAGCTTAGAGAAGAGATTTGGCCAGTCAGCAGCATTTGTTGCCTCCACTCTGATGGAATA 	TGGTGGTGTTCCTCAGTCCTCCACTCCAGAATCTCTTTGAAAGAAGCTATCCATGTCATAT	AAGTTGTGGCTATGAGGACAAGTCTGAATGGGGAACTGAGATTGGTTGG
GTTTGCTA ATTTGCTA	GTTTTACT	AGACCGCC GGAAAGAC	TTCTAAGG	CAGGAAACA CTGGGAATA	SCCTTGATA SGCTTGACA	TEGGGTTCC AGGCTTTC	rccitacta rccigacaa	AGGCTGTCC AAGCTCTTA	ATGTGCAGT	ACACTGTCT	TGGGAACTG TGGGAACAG	AGGCGAAGA AGCTGATC	CAAAGAAAA ACAAGAGTT	TATTCAATC TCTTTAACA	CAGTTCTCA 	CCTCCACTC CATCCACCI	AAGAAGCTP AGGAAGCTP	TTGGTTGG
SACTTCAGA AACTGCCGA	AGCTCCCGP AGCTCCAGP	ATTIGITAA 	TGCCCTAG1 TGCCCTTG1	ACCATGGCC 	CAGTGGTGC CAGTGGTGC	AAAGCGTCC AAAGAGACC	CTCAGCTG:	CAACAGCA TAGCAGCA	AGTCTGTT	AAACAGGAI TAATAGGAI	AGTTTATG: AGTCTATG:	CCCAATTA	AAGCAAGTO	TGTTCCAG	TGAGAAAT TGAAAGGT	ATTTGTTG	TCTTTGA TCTACTGA	AACTGAGA
TTGGCTGA CTCTCTGA	GAACCCAG 	CAGCCTTC	AGGATAAA AGAATCAA	GATGGCAC	CTTGGTCA TTGGGGCA	TCTCGTGA 	GTTCGTGT	TACATCAA TACTTCAA	AGGTCCGCA 	CGATATGC 	CAAGGACC	GAGCC GATCCTGT	BAAGAAGGC 	SGACAGTTC AGAATCTTC	STTTGATGA -TATGAGGA	STCAGCAGO	CCAGAATC CCAGCTTC	rgaatggg
TTGACGCA TTGAGTCT	ATGACATT ACAATATT	ACAAAGTC	TTAAAATC TCAAAATA	TCATGCAA	AGGTTTTC AGGTGTTC	TTTATGTG TCTATGTC	ATGCCCTI	GTGATCAC	CCAAACCTP	AGGAATGAT 	SACGGCATT	rarggrraj rarggaraj	SGGGCCAAC 	aagcatgtc aagagaaca	SGTGCTGGC	TTTGGCCA(TTTGGTCA(rcercac: rcaacaaa(SACAAGTC
GCTGACTT GCTGACTT	GAAGAAGT TAAGAAGC	CCTGAAAG 	TGAAGAAT TGAAGAAT	AGGATGGA GGGGTGGA	AATGATTO	CCGTTTAC ACGTCTTC	TGCCATG	TCTTGATT 	AATGGATC	GATTGATA CATTGACT	GGGCCTTC AGGTCTAC	AGCTATC	ACTATGTO TAAGAGC	GTCGAAC	STGTTGAA(STATTGAA	AGAAGAGA' AGAAACGC'	TTCTTCAG'	SCTATGAG
AGCTTCAAT 	ACCATITGE 	ATTGATTA 	SAGAGAATA 	CCCGAGGA GCTGAAGA	CATCCTGG	FGAGCTCCC FGAATTACC	SAAGGCTGG SAAGGCTGG	CATGTTGAA 	STGCTTCCT	STTTGATGG ATTTGATGG	TAACTTGAG	CAACAGAAC AATAGGCA	CTTGGCATC 	TAAGAAAA! CAAAGCCG	AGAGGAGGC CGAGGAGGC	GAGCTTAG2 GAAATTGG2	TGGTGGTG1 AGGTGGCA1	AAGTTGTG(
1250 A 1351 C	1310 A	1370 A 1471 A	1430 G 1531 G	1490 C	1550 T	1610 1 1711 1	1670 0	1730 C	1790 0	1850 0	1910 7	2071	2027 0	2087	2147 2251 0	2207 (2367	7
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                                                2447 TTGCATGCCCAAGCGCCCAGCTTTCAAGGGATCTGCCCCCATCAATCTTTCAGATCGTCT
                                                                                              CACCATTTACCCACTAACCTCTCTCCCGCTTCTAGTCTATTGTATATTGCCTGCTATCTG
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The present sequence encodes a maize cellulose synthase polypeptide.
The cellulose synthase can be used for the improvement of stark quality
for improved stand or singer. It also provides an increased concentration
of cellulose in the pericarp, hardening the kernel and improving its
handling ability. The sequences are used to produce transgenic plants
and seeds expressing the cellulose synthase. The polynucleotide is
used for modulating, preferably increasing, the level of the synthase
in a plant cell. The plants are preferably monocots. The polynucleotide
is also used as a probe or primer in the detection quantitation or
isolation of gene transcripts. The probes are useful in detecting
deficiencies in the level of mRNA in screenings for desired transgenic
plant, for detecting mutations in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection of any number of allelic variants of the gene,
cor for use as molecular markers in plant breeding programs. The
isolated nucleic acids of the present invention can also be used for
recombinant expression of their encoded polypeptides or for use as
immunogens in the preparation and/or screening of antibodies. The
proteins can be employed in assays for enzyme agonists or antagonists
of enzyme function or for use of immunogens or antigens to obtain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein .
                Maize; cellulose synthase; stalk quality; stand; silage; cellulose; transgenic plant; plant breeding marker; ss.
                                                                                                                                                   /*tag= a
/product= "cellulose synthase"
/note= "no termination codon given"
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                                                                                                              Location/Qualifiers 179..3397
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P-PSDB; AAY84112.
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9 53 CCGCGCCATGGACGCCGACGCCCTGAAGTCCGGGAGGCACGGGGCCGGGGACGT 112 113 GTGCCAGATCTGCGCCGACGGCCTGGGCACGTTGGACGGCGACGTCTTCACCGCCTG 172 CGACGTCTGCCGCTTTCCCGGTCTGCCGCCCCTGCTACGAGCACGAGGAGGGGCAC 232 238 CCGCCACGACGCCGACGCCCTGTCCCGGCTAAGCCCACGAAGAGTGCGAATGGGCAGGT 297 99; Gaps Score 1408.4; DB 21; Length 3725; Pred. No. 0;); Mismatches 966; Indels 99; (Sequence 3725 BP; 927 A; 807 C; 950 G; 1041 T; 0 other; . 0 38.8%; 66.8%; Best Local Similarity 66.8 Matches 2147; Conservative Query Match 173

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QY Db	233	CCAGGCCTGCCTCCAGTGCAA 	MGTACAAGCGCCACAGAGGGACCCAGCGATCCG 292
φ q	293		CCGATGATGGTAGTGACTTCAACTACCCTGCATC 352
oy y	353		41
οp	538	O	
οy	413	CGGGGCAGTGGCAATGTTGG	CCAAGTATGACAGTGGCGAGATCGGCCTCTCCAA 472
Op	575	GACGCTGATCTGTTCATCTG	cargaccacarcgarrccacgccrraca 634
οy	473	GTATGACAGTGGAGAG	CCAACAGCCAGATGTC 53
qq	635	AGTGGA	ACAGATATC 651
δŏ	es .	AGGAGAAATCCCTGGAGCTTCC	ATCATCACATGATGTCCCCTACGGGGAACATCAG 592
QQ	652		ACCGICATICTAICCGCAGICCAACAICGAGCIA 711
δō,	σ,	O I	ATCATTCACCAAATCCGTCAAGGGAGTTCTC 649
QQ	717	TGTTGATCCAAGCGTTCCAGT	-
QV Dp	650	CGGCAGTATTGGGAATGTTGCC 	AAGAGAGAGTTGATGGCTGGAAAATGAAGCAGGA 709
οy	710		GACAAGCATTGCTCCTCTGAAGGTCGGGCAGC 769
Ор	832	CAAAAATATGTTGCAAGTGACT	TAAATATCCAGAGGC 870
QY	770	TACTGACATCGATGCATCTACT	63
QQ	871	E4	PAATGGAGAAGATATGCAAATGGTTGATGATGC 930
οy	830	TCGCCAGCCTCTATCTAGAAAA	CATIGCTICCICCAAATAAATCCCTACAGAAT 889
QQ	931		AATTICITCAAACAGCICAACCITTACCGGAT 990
οy	890	GGTCATTGTTCTGCGTTGGTT	AAGCATCTTCCTGCACTACCGTCTCACAAATCC 949
ф	991		Grecricitctararaceratearcated 1050
δλ	950	TGTGCGTAATGCATACCCACTG	TTTATCTGTTATATGTGAGATTTGGTTTGCTTT 1009
qq	1051	AGTGCGTAATGCATT	AGTATCTGTTATCTGTGTGTTTGCCTT 1110
ΟŊ	1010	ATCCTGGATACTGGATCAGTTC	GIGGITICCAATCAACCGGGAGACCTACCTIGA 1069
Ωp	1111		ATGGTATCCAATCAACCGTGAGACATATCTCGA 1170
Qγ	1070	TAGACTGGCTTTAAGGTATGAC	AGGTGAACCGTCTCAGTTGGCTGTTGACAT 1129
qq	1171		GGGAGAGCCATCACAGCTGGCTCCCATTGATGT 1230
ΟŊ	1130	ATTTGTCAGTACAGTCGACCCC	GGAGCCACCTATCGTCACTGCCAACACTGTGCT 1189
qq	1231		GGAACCTCCACTGATCACAGCCAACACTGTTT 1290
δλ	1190	AICCAIICIIGCIGIIGAIIAI	GGACAAGGTCTCTTGCTATGTATCTGATGACGG 1249
Op	1291		TGACAAAGTGTCATGTTTCTGATGATGG 1350
QY	1250	AGCTTCAATGCTGACTTTTGAC	GGCTGAGACTTCAGAGTTTGCTAGGAAATGGGT 1309
q	1351		CTCTGAAACTGCCGAATTTGCTAGAAAGTGGGT 1410
QY	1310	ACCATTTGTGAAGAAGTATGAC	ACCCAGAGCTCCCGAGTTTTACTTTTGCCAGAA 1369

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                          AATTGATTACCTGAAAGACAAAGTCCAGCCTTCATTTGTTAAAGACCGCCGGGCCATGAA
                                             AATAGATTACCTGAAGGACAAAATTCAACCTTCATTTGTTAAGGAAAGACGAGCAATGAA
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Maize; cellulose synthase; stalk quality; stand; silage; cellulose; transgenic plant; plant breeding marker; ss.
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                                                                                                             TCTGCTCACTGGAAAGTTCATCATGCCAGAGATTAGCAACTTGGCCAGTATCTGGTTCAT
                                                                                                                                         TGCGCTCTTCCTTTCAATTTTCGCCACTGGTATCCTTGAGATGAGGTGGAGTGGTTTGG
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                                            GAACCAAGTGCTGCGGTGGGCTCTCGTTCTTTGAAATTCTTTTCAGCCGGCATTGCCC
                                                                        CTTATGGTATGGCTACGGAGGCGCCCTCAAGTTCCTGGAGAGATTCGCTTACATCAACAC
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genes which encode maize cellulose synthase polypeptides in plants iul for modulating the expression of cellulose synthase in plants to produce transgenic plants expressing the novel protein -
                  /*tag= a
/product= "cellulose synthase"
/note= "no termination codon given"
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                                                                                                                 Wang
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     Location/Qualifiers
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                                                                        16-AUG-1999;
                                                                                     17-AUG-1998;
                                                                                                                Dhugga KS,
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The present sequence encodes a maize cellulose synthase polypeptide. The cellulose synthase can be used for the improvement of stalk quality for improved stand or silage. It also provides an increased concentration of cellulose in the pericarp, hardening the kernel and improving its handling ability. The sequences are used to produce transgenic plants and seeds expressing the cellulose synthase. The polynucleotide is used for modulating, preferably increasing, the level of the synthase in a plant cell. The plants are preferably monocots. The polynucleotide is salso used as a probe or primer in the detection quantitation or isolation of gene transcripts. deficiencies in the level of mRNA in screenings for desired transgenic plant, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants of the gene, or for use as molecular markers in plant breeding programs. The isolated nucleic acids of the present invention can also be used for recombinant expression of their encoded polypeptides or for use as immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.

Sequence 3725 BP; 927 A; 807 C; 950 G; 1041 T; 0 other;

9 GIGCCAGAICTGCGCCGACGCCTGGGCACCACGTTGGACGGCGACGTCTTCACCGCCTG 172 CCAGGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGCCACAGAGGGAGCCCAGCGATCCG 292 CCAATGCTGCCCTCAGTGCAAGACTAGATACAAGAGACAGAAAGGTAGCCCTCGAGTTCA 477 CGGGGAGGAAGGCGACGACACTGATGCCGATGATGGTAGTGACTTCAACTACCCTGCATC 352 CCGCGCCATGGACGCGGACGCCCTGAAGTCCGGGAGGCACGGGGCCGGGGACGT 112 CCGCCACGACGCGACGCGCCTGTCCCGGCTAAGCCCACGAAGAGTGCGAATGGGCAGGT 297 99; Gaps CGACGTCTGCCGCTTCCCGGTCTGCCGCCCTGCTACGAGCACGAGGAGGAGGGCCAC Score 1408.4; DB 21; Length 3725; Pred. No. 0; 966; Indels ed. No. 0; Mismatches ; 0 38.8%; 66.8%; Best Local Similarity 66.8 Matches 2147; Conservative 113 293 53 238 298 173 358 233 a g g à à à g ò

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AGTATCTGTTATCTGTGAGGTCTGGTTTGCCTT 1110 AGGTGAACCGTCTCAGTTGGCTGTTGACAT 1129 ACCCAGAGCTCCCGAGTTTTACTTTTGCCAGAA 1369 STGGTTTCCAATCAACCGGGAGACCTACCTTGA 1069 SGGAGAGCCATCACAGCTGGCTCCCATTGATGT 1230 GCCTTCATTTGTTAAAGACCGCCGGGCCATGAA 1429 AAATGGAGAAGATATGCAAATGGTTGATGATGC 930 CATTGCTTCCTCCAAAATAAATCCCTACAGAAT 889 TGCTGACAGGATGCGCAGCTGGCGCATGAACAC 412 CCGTCATTCTATCCGCAGTCCAACATCGAGCTA 711 ------ACAGATATC TCATCACATGATGTCCCCTACGGGGAACATCAG AGAGAGAGTTGATGGCTGGAAAATGAAGCAGGA -----TAATATCCAGAGGC CATGACCCACACCATCGGATTCCACGCCTTACA GAGGATTGTGGACCCCTCGAAGGACTTGAATTC GGAAAGAGTTGAGAGCTGGAGGGTTAAACAGGA AATTTCCTCAAACCAGCTCAACCTTTACCGGAT CAAGTATGACAGTGGCGAGATCGGCCTCTCCAA SATACGTCCCTTCAGTCACCAACAGCCAGATGTC CAACATGGAAGACGCTTTACTGAATGATGAAAC **AAGCATCTTCCTGCACTACCGTCTCACAAATCC** GGACAAGGTCTCTTGCTATGTATCTGATGACGG TCATTCACCAAATCCGTCAAGGGAGTT---CTC GACAAGCATTGCTCCTCTGAAGGTCGGGCAGC TTTATCTGTTATATGTGAGATTTGGTTTGCTTT GGAGCCACCTATCGTCACTGCCAACACTGTGCT SGCTGAGACTTCAGAGTTTGCTAGGAAATGGGT CTCTGAAACTGCCGAATTTGCTAGAAAGTGGGT AATTGATTACCTGAAAGACAAA AGCTTCAATGCTGACTTTTGAC ACCATTTGTGAAGAAGTATGAC TCCCTTTTGTAAGAAGCACAAT 772 CTATGGGCTTAATAGTGTTGAG 1070 TAGACTGGCTTTAAGGTATGAC ATCCATTCTTGCTGTTGATTAT GTCCATTCTTGCTGTGGATTAC TGGTGATGATGAGGAGGAAGAT TGGCACTGAGGACCAGAAGCA 413 CGGGGCAGTGGCAATGTTGG 575 GACGCTGATCTGTCTTCATCT GTATGACAGTGGAGAGATCCC 533 AGGAGAATCCCTGGAGCTTC CGGCAGTATTGGGAATGTTGCC CAAGGGTGCGATTCCCCATGACI TACTGACATCGATGCATCTACT 830 TCGCCAGCCTCTATCTAGAAA 991 AGTAATCATICTCCGTCTTATC 1171 CAGGCTTGCATTGAGGTATGAI 1130 ATTTGTCAGTACAGTCGACCCC CTTTGTCAGTACAGTGGATCC CTCAGCTATGCTGACTTTTGAG CAATGGGAAGGGCCCCAGAGTG 593 CAGACGIGCICCGITICCCIA TGTTGATCCAAGCGTTCCAGT CAAAAATATGTTGCAAGTGAC 871 TAGAGGAGACATGGAGGGGAC 931 ACCCCTACCTTTGAGCCGCAT 1051 AGTGCGTAATGCTTATGGATT GGTCATTGTTCTGCGGTTGGT TGTGCGTAATGCATACCCACT ATCCTGGATACTGGATCAGTT 635 AGTGGACA-----1231 1351 353 473 712 650 710 832 770 890 1190 1291 1250 1370 1411 셤 a g a g g ò g δ 셤 ò οŽ 셤 $Q_{\underline{Y}}$ ò à 음 οy ò 염 οy a Óγ g g g à δ ò ò ά В ŏ g ò

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AATAGATTACCTGAAGGACAAAATTCAACCTTCATTTGTTAAGGAAAGACGAGCAATGAA 1530
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                                                                                   TCTGCTCACTGGAAAGTTCATCATGCCAGAGATTAGCAACTTGGCCAGTATCTGGTTCAT
                                                                                          2785 ICTTCTTACCAATAAATTTATCATTCCTGAGATTAGTAATTATGCTGGAATGTTCTTCAT
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GAACCAAGTGCTGCGGTGGGCTCTCGGTTCTTGAAATTCTTTTTCAGCCGGCATTGCCC
                            CTTATGGTATGGCTACGGAGGCGCCTCAAGTTCCTGGAGAGATTCGCTTACATCAACAC
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Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic pathway; transgenic plant; ds.

WO200022092-A2 Pinus radiata

20-APR-2000

Pinus radiata cellulose synthase nucleotide sequence SEQ ID NO:69

Page

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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences, sequences at least 50% identical to them. 200, 100, 40 or 20-mers of the 835 sequences or sequences that are degenerately equivalent or allelic to the 835 sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the present invention.
                                                                                                                                                                                                                                                                                 New genes encoding proteins involved in a plant polysaccharide blosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3851 BP; 1040 A; 796 C; 944 G; 1071 T; 0 other;
                                                                                                                    (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 71-72; 301pp; English.
                                                        98US-0170862
99US-0148426
                 99WO-NZ00169
                                                                                                                                                                                                                   WPI; 2000-339328/29.
P-PSDB; AAB16307.
                                                                                                                                                                                Bloksberg LN
                 08-OCT-1999;
                                                        13-OCT-1998;
11-AUG-1999;
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515 575 492 689 194 314 374 635 552 GAGGAGCCGAAGCCTTTGAACACGTTGAGCCCACGTCTGCCCAGATTTGTGGCGAGGAC 281 TGCCGCCCCTGCTACGAGCACGAGGGCGAAGGAGGCCACCCAGGCCTCCAGTGCAAG 254 401 434 GACGCCCTGAAGTCCGGGAGGCACGGGGCCGGGGACGTGTGCCAGATCTGCGCCGACGGC 134 Gaps CTGGGCACCACGTTGGACGCGACGTCTTCACCGCCTGCGACGTCTGCCGCTTCCCGGTC ACCAAGTACAAGCGCCACAGAGGGAGCCCAGCGATCCGCGGGGGAGGAAGGCGACGACACT GATGCCGATGATGGTAGTGACTTCAACTACCCTGCATCTGGCACTGAGGACCAGAAGCAG GAAGACGTTGATGACATAGAACATGAATTTAATGTGGAGACTCAGCAAAGAAACAGGCAG AAGATTGCTGACAGGATGCGCAGCTGGCGCATGAACACCGGGGGGCAGTGGTTGGC 435 CACCCCAAGTATG-ACAGTGGCGAGATCGGCCTCTCCA-AGTATGACAGTGGAGAGATCC CTAGGGGATACGTCCCTTCAGTCACCAACAGCCAGATGTCAGGAGAAATCCCTGGAGCTT CACTCGGTTGTGAGTGGGGAGATTCCAACGTCATACTACGCAGACAACCAATTG-----Length 3851; 38.1%; Score 1382; DB 21; llarity 66.4%; Pred. No. 0; Conservative 0; Mismatches 1040; Best Local Similarity Matches 2142; Conserv Query Match 135 255 516 75 222 282 195 342 315 456 375 493 989 402 g 셤 g δ a qq g g ò ò ò Ωý ò ò qq δ

069	CTTGCCAACCCTGCAATGC	CAAGCTCCGAGCCGGGAGTGGA 74
7 3	ATGTGAATCATTCACCAAATCC	GGGAGTTCTCCGGCAGTATTGGGAATGTTGCCT 672
ന വ	GGAAAGAGAGAGTTGATGGCTG 	TGAAGCAGGACAAGGGTGCGATTCCCATGACTA 732
33 65	ATGGGACAAGCATTGCTCCCTC	GTCGGCAGCTACTGACATCGATGCATCTACTG 792
93	AATACAACATGGAAGACGCTTT 	ATGATGAAACTCGCCAGCCTCTATCTAGAAAG 852
53	TCCCCATTGCTTCCTCCAAAAT 	CCTACAGAATGGTCATTGTTGCGGGTTGGTTG 912
13 36	TTCTAAGCATCTTCCTGCACTA	TCACAAATCCTGTGCGTAATGCATACCCACTGT 972
73	GGCTTTTATCTGTTATATGTGAE	GGTTTGCTTTATCCTGGATACTGGATCAGTTCC 1032
33	CGAAGTGGTTTCCAATCAACCG6 CCAAGTGGTTGCTATCAGTCG7	CCTACCTIGATAGACTGGCTTTAAGGTATGACC 1092
093 216	GAGAAGGIGAACCGICTCAGTIG 	TIGITGACATATITGICAGFACAGTCGACCCT 1152
153 276	TGAAGGAGCCACCTATCGTCACT	ACACTGTGCTATCCATTCTTGCTGTTGATTATC 1212
213 336	CCGTGGACAAGGTCTCTTGCTAT	TIGATGACGGAGCTTCAATGCTGACTTTTGACG 1272
73	CATTGGCTGAGACTTCAGAGTT7 	SGAAATGGGTACCATTTGTGAGAAGTATGACA 1332
33	TTGAACCCAGAGCTCCCGAGTTT 	TITGCCAGAAAATIGATTACCIGAAAGACAAAG 1392
93	TCCAGCCTTCATTTGTTAAAGAC 	rggccatgaagagaatatgaagaatttaaaa 1452
453 576	TCAGGATAAATGCCCTAGTTTCT 	ATTGAAAGTCCCCGAGGAAGGATGGATCATGC 1512
513 636	AAGATGGCACACCATGGCCAGGA	ATACCAGGATCATCCTGGAATGATTCAGGTTT 1572
73	TCCTTGGTCACAGTGGTGGCCTT	TGAGGGTAATGAGCTCCCCCGTTTAGTTTATG 1632
33	TGTCTCGTGAAAACGTCCTGGG TTTCTCGTGAGAAGACCTGGT	SCACCACAAGAAGGCTGGTGCCATGAATGCCC 1692

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CGCCTGATCATCATGATGTCCCCTACGGGGAACATCAGGAGACGTGCTCGGTTTCCCT 612

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         CAGCAGCATTTGTTGCCTCCACTCTGATGGAATATGGTGGTGGTGCTCCTCAGTCCTCCACTC
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TIGITCGTGTCTCAGCTGTCCTTACTAATGGACAATACATGTTGAATCTTGATTGTGATC
                                 ACTACATCAACAACAACAAGGCTGTCCGAAGAGCTATGTGCTTCCTAATGGATCCAAACC
                                                  ACTACATTAACAATAGCAAGGCAATCAGGGAAGGCATGTGCTTTATGATGGATCCTCAGG
                                                                  TAGGTCCGCAAGTCTGTTATGTGCAGTTCCCACAAAGGTTTGATGGGATTGATAGGAATG
                                                                            ATCGATATGCAAACAGGAACACTGTCTTTTTGATATTAACTTGAGGGGCCCTTGACGGCA
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snic plant; plant breeding marker; ss.
                                                 2941 AGTICTGGGTTATTGGAGGGTTTCTGCACATTTTTTTGCAGTTATTCAAGGCTGCACA
                                                                                         GCGACTTTGCTGAGCTCTACATGTTCAAGTGGACGACGCTTCTCATCCCTCCGACGACCA
                                                                                                                                                                         ACCAATCATGGGGGCCGCTCTTTGGGAAGCTCTTCTTTGCCTTCTGGGTGATTGTTCACT
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            AGTTCTGGGTCATTGGAGGTATCTCTGCACATCTGTTTGCCGTCTTTCAGGGTCTTCTGA
                                                                              AGGTGCTTGCCGGTATCGACACCAACTTCACTGTCACCTCAAAGGCTAATGACGAAGAAG
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CTGGTATCCTTGAGATGAGGTGGAGTGGTGTTGGCATTGACGAGTGGTGGAGGAATGAAC
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/product= "cellulose synthase"
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The present sequence encodes a maize cellulose synthase polypeptide.
The cellulose synthase can be used for the improvement of stalk quality
for improved stand or sliage. It also provides an increased concentration
of cellulose in the pericarp, hardening the kernel and improving its
handling ability. The sequences are used to produce transgenic plants
and seeds expressing the cellulose synthase. The polymuleotide is
used for modulating, preferably increasing, the level of the synthase
in a plant cell. The plants are preferably monocots. The polymucleotide
is also used as a probe or primer in the detection quantitation or
isolation of gene transcripts. The probes are useful in detecting
deficiencies in the level of mRNA in screenings for desired transgenic
plant, for detecting mutations in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection of any number of alielic variants of the gene,
or for use as molecular markers in plant breeding programs. The New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein isolated nucleic acids of the present invention can also be used for recombinant expression of their encoded polypeptides or for use as immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein. Claim 1; Page 144-149; 119pp; English. P-PSDB; AAY84115.

Sequence 3753 BP; 944 A; 805 C; 965 G; 1038 T; 1 other;

1; CCGCGCCATGGACGCGGACGCCCTGAAGTCCGGGAGGCACGGGGCCGGGGACGT 112 GIGCCAGATCIGCGCCGACGGCCTGGGCACGTIGGACGGCGACGTCTTCACCGCCTG 172 CCAATGCTGCCCCCAGTGCAAGACTAGATACAAGAGACAGAAAGGTAGCCCTCGAGTTCA 482 TGGCACTGAGGACCAGAAGCAGAAGATTGCTGACAGGATGCGCAGCTGGCGCATGAACAC 412 CGGGGGCAGTGGCAATGTTGGCCACCCCAAGTATGACAGTGGCGAGATCGGCCTCTCCCAA 472 CAGACGTGCTCCGTTTCCCTATGTGAATCATTCACCAAATCCGTCAAGGGAGTTC---TC 649 Gaps CCAGGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGCCACAGAGGGAGCCCAGCGATCCG 243 CCGCCACGACGCGATGTGCCGGGCTCGGCTAAGCCCACAAAGAGTGCGAATGGACAGGT CGACGTCTGCCGCTTCCCGGTCTGCCGCCCTGCTACGAGCACGAGCGCAAGGAGGGCCAC CGGGGAGGAAGGCGACACTGATGCCGATGATGGTAGTGACTTCAACTACCCTGCATC 483 TGGTGATGAGGATGAGGAAGATGTTGATGACCTAGACAAGAATTCAACTAC---------AAGCAAGGC 544 AGTGGGAAAGGCCCAGAGTGGCAACTGCAAG---GAGATGATGCTGATCTGTTTCATCT GTATGACAGTGGAGATCCCTAGGGGATACGTCCCTTCAGTCACCAACAGCCAGATGTC GCTCGCCATGAGCCACATCATCGGATTCCACGCCTGACAAGCGGTCAA----CAGATATC AGGAGAAATCCCTGGAGCTTCGCCTGATCATCACATGATGTCCCCTACGGGGGAACATCAG 96; Score 1373; DB 21; Length 3753; Pred. No. 0; 0; Mismatches 986; Indels 96; 37.9%; Best Local Similarity 66.3 Matches 2130; Conservative Query Match 413 53 173 363 233 423 293 353 473 601 593 ŏ q d g g qq q 쉽 à à q ŏ ò ò В Š à ò ò

ACCCAGAGCTCCCGAGTTTTACTTTTGCCAGAA 1369 GCCACACCATGGCCAGGAAACAATACCAGGGA 1549 GGTCACAGTGGTGGCCTTGATACTGAGGGTAA 1609 CGTGAAAAGCGTCCTGGGTTCCAGCACCACAA 1669 CGTGAAAAGAGACCAGGCTTTCAGCATCACAA 1778 CGTGTCTCAGCTGTCCTTACTAATGGACAATA 1729 AGAGAGAGTTGATGGCTGGAAAATGAAGCAGGA 709 CTCAGAAACCGCAGAATTTGCTAGAAAGTGGGT GAGGATTGTGGACCCCTCGAAGGACTTGAATTC GTGCTTCTTCCAGTATCGTGTCAGTCATCC GGACAAGGTCTCTTGCTATGTATCTGATGACGG SCCTTCATTTGTTAAAGACCGCCGGGCCATGAA GACAAGCATTGCTCCCTCTGAAGGTCGGGCAGC ATATCCAGAGGCTAGAGGAGGACATGGAGGG CAACATGGAAGACGCTTTACTGAATGATGAAAC -----GAANATATGCAAATGGTTGATGC CATTGCTTCCTCCAAAATAAATCCCTACAGAAT AATTTCCTCAAACCAGCTCAACCTTTACCGGGT AAGCATCTTCCTGCACTACCGTCTCACAAATCC TITATCTGTTATATGTGAGATTTGGTTTGCTTT AGTATCTGTTATCTGCGAGGTCTGGTTTGCCTT STEGITTCCAATCAACCGGGAGACCTACCTTGA AGGTGAACCGTCTCAGTTGGCTGCTGTTGACAT SGAGCCACCTATCGTCACTGCCAACACTGTGCT GGAACCTCCACTGATCACAGCCAACACTGTTTT SGCTGAGACTTCAGAGTTTGCTAGGAAATGGGT GATAAATGCCCTAGTTTCTAAGGCATTGAAAGT GAAGGCTGGTGCCATGAATGCC 1299 GICCALICILICIGGGALTAC 1310 ACCATTTGTGAAGAAGTATGAC CCCCGAGGAAGGATGGATCATG GCCTGAAGAGGGGTGGACCATG 1550 TCATCCTGGAATGATTCAGGTT AGCTICAATGCTGACTTTTGAC 1359 TTCAGCTATGCTGACTTTTGAG 1419 TCCCTTTTGTAAGAAGCACAAT 1370 AATTGATTACCTGAAAGACAAA GAGAGAATATGAAGAATTTAAA 1539 GAGGGAGTATGAAGAATTCAAA CCATCCTGGCATGATTCAGGTT 1610 TGAGCTCCCCCGTTTAGTTTAT 1719 TGAGTTACCACGTCTTGTCTAT 1070 TAGACTGGCTTTAAGGTATGAC 1130 ATTTGTCAGTACAGTCGACCCC CTTCGTCAGTACAGTGGATCCA 1190 ATCCATTCTTGCTGTTGATTAT TCGCCAGCCTCTATCTAGAAA 939 ACGCTACCTTTGAGCCGTATC 999 AGIGATCATICICCGICTIAIC 1010 ATCCTGGATACTGGATCAGTTC CGGCAGTATTGGGAATGTTGC 710 CAAGGGTGCGATTCCCATGACT 770 TACTGACATCGATGCATCTAC 1179 CAGGCTTGCATTGAGGTATGA 717 TGTTGATCCAAGCGTCCCAGT CTATGGGCTTAATAGTGTTGA CAAAAATATGATGCAAGTGAC GGTCATTGTTCTGCGGTTGGT 950 TGTGCGTAATGCATACCCACT AGTGCGTGATGCTTATGGATT 897 GACTGGCTCAAATGGA---1599 1059 1430 1490 650 837 890 1659 ò q δ Q Qγ q ò g ò q Ω 셤 9 g ò g ŏ g δ g ŏ qq δy qq δ g QΥ Ω ò g οy g δ

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/product= "cellulose synthase"
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plants for modulating the expression of cellulose synthase in produce transgenic plants expressing the novel protein and to

Claim 1; Page 184-188; 119pp; English

The present sequence encodes a maize cellulose synthase polypeptide.

The cellulose synthase can be used for the improvement of stalk quality

Comproved stand or silage. It also provides an increased concentration

of cellulose in the perioarp, hardening the kernel and improving its

nandling ability. The sequences are used to produce transgenic plants

compared for modulating, preferably increasing, the polynucleotide is

consed for modulating, preferably increasing, the level of the synthase

consed for modulating, preferably increasing, the level of the synthase

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consediction of an a probe or primer in the detection quantitation or

colation of gene transcripts. The probes are useful in detecting

deficiencies in the level of mRNA in screenings for desired transgenic

colation of gene transcripts. The probes are useful in detecting

confection of gene transcripts. The probes are useful in detecting

confection or changes in enzyme activity in screening assays of

compounds, for detection of any number of allelic variants of the gene,

compounds, for detection of any number of allelic variants of the gene,

confection or changes in enzyme activity in screening assays of

confections an obtending of the present invention can also be used for

recombinant expression of their encoded polypeptides or for use as

confections can be employed in assays for enzyme agonists or antagonists

confections can be employed in assays for enzyme agonists or obtain

confections are also antagonists or solution of confective with a protein.

Sequence 3753 BP; 944 A; 805 C; 965 G; 1038 T; 1 other;

Gaps 96; Length Indels DB 21; Pred. No. 0; 0; Mismatches 986; Score 1373; I 37.9%; 66.3%; 3est_Local Similarity 66.3
4atches 2130; Conservative Query Match

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AGGAGAAATCCCTGGAGCTTCGCCTGATCATCACATGATGTCCCCTACGGGGAACATCAG 592 CCGCGCCATGGACGCGACGCGGACGCCCTGAAGTCCGGGAGGCACGGGGCCGGGGACGT 112 GIGCCAGATCIGCGCCGACGCCTGGGCACCACGTTGGACGCCGACGTCTTCACCGCCTG 172 CAATGAGTGTGCCTTCCCTGTCTGCCGCCCATGCTATGAGTATGAGCGCAAGGGGGGAA 422 CCAGGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGCCACAGAGGGAGCCCAGCGATCCG 292 TGGCACTGAGGACCAGAAGCAGAAGATTGCTGACAGGATGCGCAGCTGGCGCATGAACAC 412 CGGGGGCCAGTGGCCATGTTGGCCCACCCCAAGTATGACAGTGGCGAGATCGGCCTCTCCAA 472 GTATGACAGTGGAGAGATCCCTAGGGGATACGTCCCTTCAGTCACCAACAGCCAGATGTC 532 TGGAGAGATTCCTGATGCTTCCCCTGACCGTCATTCTATCCGCAGTCCAACATCGAGCTA 716 TGTTGATCCAAGCGTCCCAGTTCCTGAGGATTGTGGACCCCTCGAAGGACTTGAATTC 776 CGGGGAGGAAGGCGACGACACTGATGCCGATGATGGTAGTGACTTCAACTACCCTGCATC TGGTGATGAGGATGATGTTGATGACCTAGACAATGAATTCAACTAC-----GCTCGCCATGAGCCACATCATCGGATTCCACGCCTGACAAGCGGTCAA----CAGATATC CAGACGTGCTCCGTTTCCCTATGTGAATCATTCACCAAATCCGTCAAGGGAGTTC---TC 53 303 353 243 113 173 363 423 293 413 544 473 601 657 717 q Dp Dp Ω ð ò ò g δ ŏ Q ŏ g à g ò g ã ò

NGTGGTTTCCAATCAACCGGGAGACCTACCTTGA 1069 rggrcacagrggrgccrrgaracrgagggraa 1609 TCGTGAAAAGCGTCCTGGGTTCCAGCACCACAA 1669 TCGTGTCTCAGCTGTCCTTACTAATGGACAATA 1729 TCGTGTATCTGCTGTGCTGACAATGGTGCCTA 1838 ITGACAAAGIGICAIGCIAIGIITCIGAIGAIGG 1358 CATCAACAACAGCAAGGCTGTCCGAGAAGCTAT 1789 896 889 AAGAGAGAGTTGATGGCTGGAAAATGAAGCAGGA PGTGCTTCTTCCAGTATCGTGTCAGTCATCC AGGGAGAGCCATCACAGCTGGCTCCCATTGATGT FGGCTGAGACTTCAGAGTTTGCTAGGAAATGGGT AACCAAGAGCTCCAGAATTTTACTTTGCTCAAAA SGACAAGCATTGCTCCCTCTGAAGGTCGGGCAGC **NATATCCAGAGGCTAGAGGAGGAGACATGGAGGG** -----GAANATATGCAAATGGTTGATGC CCATTGCTTCCTCCAAAATAAATCCCTACAGAAT CAATTTCCTCAAACCAGCTCAACCTTTACCGGGT **ITTIATCTGTTATATGTGAGATTTGGTTTGCTTT AAGGTGAACCGTCTCAGTTGGCTGCTGTTGACAT** GGAGCCACCTATCGTCACTGCCAACACTGTGCT reteagaaacegeagaatttgetagaaagtgggt ACCCAGAGCTCCCGAGTTTTACTTTTGCCAGAA GATAAATGCCCTAGTTTCTAAGGCATTGAAAGT TGGCACACCATGGCCAGGAAACAATACCAGGGA ACAACATGGAAGACGCTTTACTGAATGATGAAAC TARGCATCTTCCTGCACTACCGTCTCACAAATCC GGACAAGGTCTCTTGCTATGTATCTGATGACGG GCCTTCATTTGTTAAAGACCGCCGGGCCATGAA CAAAAATATGATGCAAGTGAC 1130 ATTTGTCAGTACAGTCGACCC TTCAGCTATGCTGACTTTTGA AATTGATTACCTGAAAGACAA AATAGATTACCTGAAGGACAA GAGAGAATATGAAGAATTTAA GAGGGAGTATGAAGAATTCAA TGAGCTCCCCCGTTTAGTTTA TGAGTTACCACGTCTTGTCTA CATGTTGAATCTTGATTGTGA CGGCAGTATTGGGAATGTTGC CTATGGGCTTAATAGTGTTGA CAAGGGTGCGATTCCCATGAG TACTGACATCGATGCATCTAC TCGCCAGCCTCTATCTAGAAA 939 ACGCTACCTTTGAGCCGTAT GGTCATTGTTCTGCGGTTGGT 999 AGTGATCATTCTCCGTCTTAT TGTGCGTAATGCATACCCACT 1070 TAGACTGCCTTTAAGGTATGA 1179 CAGGCTTGCATTGAGGTATGA ATCCATTCTTGCTGTTGATTA GTCCATTCTTTCTGTGGATTA 1250 AGCTTCAATGCTGACTTTTGA 1310 ACCATTTGTGAAGAAGTATGA TCCCTTTTGTAAGAAGCACAA CCCCGAGGAAGGATGGATCAT GCCTGAAGAGGGGTGGACCAT 1550 TCATCCTGGAATGATTCAGGT CCATCCTGGCATGATTCAGGT GAAGGCTGGTGCCATGAATGC GAAGGCTGGTGCAATGAATGC GTCTTGGCTTCTAGATCAGT GACTGGCTCAAATGGA----1010 ATCCTGGATACTGGATCAGT 1190 1419 1479 1539 650 111 710 837 770 897 890 950 1119 1490 1599 1659 1610 1670 1730 g g a q g g ద g ద 셤 q g à δ ğ ò ò ŏ οy à g ŏ δ g δ ò g δ g Ω 8 δŽ g οy ò

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/product= "cellulose synthase"
/transl_except= (pos: 933..935, aa: Xaa)
/note= "no termination codon given; Xaa
unspecified amino acid"
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Claim 1;

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The present sequence encodes a maize cellulose synthase polypeptide.

The cellulose synthase can be used for the improvement of stalk quality for improved stand or silage. It also provides an increased concentration of cellulose in the pericarp, hardening the kernel and improving its handling ability. The sequences are used to produce transgenic plants and seedse expressing the cellulose synthase. The polywouclectide is used for modulating, preferably increasing, the level of the synthase in a plant cell. The plants are preferably monocots. The polywouclectide is used for modulating, preferably increasing, the level of the synthase in a plant cell. The plants are preferably monocots. The polymouclectide is also used as a probe or primer in the detection quantitation or isolation of gene transcripts. The probes are useful in detecting deficiencies in the level of mRNA in screenings for desired transgenic deficiencies in the level of mRNA in screening for desired transgenic of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants of the gene, for use as molecular markers in plant breeding programs. The isolated nucleic acids of the present invention can also be used for recombinant expression of their encoded polypeptides or for use as immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. [ toasea: l to 3763, Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design of
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2572.2 2402 2199 1373.2 1320.4 1319.8

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one_lib="Maize
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                               GGGGCAAGAAGAAGGCAAGCAAGTCAAAGAAAAGGAGCTCAGATAAGAAAAAGTCGAACA
                                                             AGCATGTGGACAGTTCTGTTCCAGTATTCAATCTCGAAGACATAGAGGAGGGTGTTGAAG
                                                                       GTGCTGGGTTTGATGATGAGAAATCAGTTCTCATGTCTCAAATGAGCTTAGAGAAGAGAT
                                                                                                       CCTCCACTCCAGAATCTCTTTTGAAAGAAGCTATCCATGTCATAAGTTGTGGCTATGAGG
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
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                                                          ACAGTGGTTACCAATCATGGGGGCCGCTCTTTGGGAAGCTCTTCTTTGCCTTCTGGGTGA 3123
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
Unpublished (2002)
2 (bases 1 to 3728)
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. 3728
/organism="Zea mays"
/db_xref="Maizebb:630049"
/db_xref="Maizebb:630049"
/db_xref="Taxon:4577"
/clone="CLil60_1"
Library"
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Pred. No. 0;
0; Mismatches 631; Indels
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clade; Panicoideae; Andropogoneae; 2ea.
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mRNA sequence
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Best Local Similarity 80.7%;
Matches 2660; Conservative (
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oد	y 396 AGCTGGCGCATGAACACCGGGGGCAGTGGCAATGTTGGCCACCCCAAGTATGACAGTGGC 455	Qy Db	AAGGCATTGAAAGTCCCCGAG AGGCACNNNNGTCCCTGAG
۵. د	Y 456 GAGATCGGCCTCTCCAAGTATGACAGTGGAGAGATCCCTAGGGGATACGTCCTTCAGTC 515	Qy	
>- O	9 516 ACCAACAGCCAGATGTCAGGAGAAATCCCTGGAGCTTCGCCTGATCATCATGATGTCC 575 1	Qy Db	
~ 0	y 576 CCTACGGGGAACATCAGCAGACGTGCTCCGTTTCCCTATGTGAATCATTCACAAATCG 635	QQ DD	
>- 0	y 636 TCAAGGGAGTTCTCCGGCAGTATTGGGAATGTTGCCTGGAAAGAGAGAG	δδ O	
>- o	y 696 AAAATGAAGCAGGACAAGGGTGCGATTCCCATGACTAATGGGACAAGCATTGCTCCCTCT 755	oy oy	
5- O	756 GAAGGTCGGCCAGCTACTGACATCGATGCATCTACTGAATACAACATGGAAGACGCTTTA 815 1	QV	
~ 0	### 816 CTGAATGAAACTCGCCGGCCCTCTATCTAGAAAAGTCCCCATTGCTTCCTCCAAAATA 875 1	QQ Db	
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5- O	996 ATTTGGTTTGCTTTATCCTGGATACTGGATCAGTTCCCGAAGTGGTTTCCAATCAACCGG 1055	VQ da	
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Tracheophyta;
ceae; PACC
                                                                                                                                                                                                                                                                                                              Joses this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project 766 c 880 g 945 t 274 others
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/clone_lib="Malze Mapping Project/DuPont Cornsensus
Library"
                                                                                                             Design
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Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Desi-
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Unpublished (2002)
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/db_xref="taxon:4577"
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Submitted (25-APR-2002) Maize
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Location/Qualifiers
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/organism="Zea mays"
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Qy Dp	2138 2320	CGAAGACATAGAGGAGGGTGT 	STGCTGGGTTTGATGATGAGAAATCAGTTCTCAT 2197
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Q.Y	2318	CCATGTCATAAGTTGTGGCTAJ 	ACAAGTCTGAATGGGGAACTGAGATTGGTTGGA 2377
ζζ Gp	2378	CTATGGATCTGTCACAGAGA1 	FTACTGGATTCAAGATGCACGCAAGAGGCTGGCG 2437
QY Dp	2438	TTCAGTCTATTGCATGCCCAAG	SAGUTITCAAGGGAICIGCCCCCATCAAICTIIC 2497
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O.y D.b	2558 2740	GCATTGCCCCTTATGGTATGG	SAGGGCCTCAAGTTCCTGGAGATTCGCTTA 2617
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/clone="CL1166_1"
/clone="Lib="Maize Mapping Project/DuPont Cornsensus Library"
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Analory.C.F., Dolan, M., Mido,G.H., Vogel,J.M., Whitsitt,M.S., Arthur.L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
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                                                                                                                                GAAGCTCTTCTTTGCCTTCTGGGTGATTGTTCACTTATACCCATTCCTCAAGGGTCTTAT
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                                                                                                                                                                CGTTGCTGGCACCTCCTACGCCATCAACAGTGGTTACCAATCATGGGGGCCGCTCTTTGG
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Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1. 3898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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sequence.
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Zea mays CL1166_1 mRNA
AY110415
AY110415.1 GI:21214824
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Unpublished (2002)
2 (bases 1 to 3898)
Coe, E.C.
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Zea mays
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VERSION
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ORGANISM
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TITLE
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AY110415
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contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project" 81 1054 t 80 others
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                                                                                                                                                                                                                                                                                                                                                                                    173 CGACGICTGCCGCTICCCGGTCTGCCGCCCTGCTACGAGCACGAGCGCAAGGAGGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTATGGGCTTAATAGTGTTGACTGGAAGGAAAGAGTTGAGAGCTGGAGGGTTAAACAGGA
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                                                                                                                                            DB 11; Length 3898;
                                                                                                                                                                                   98;
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                                                                                                                                                               Pred. No. 0;
0; Mismatches 1005;
                                                                                                                                              Score 1373.2;
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                                                                                                                                          Query Match 37.9%;
Best Local Similarity 65.7%;
Matches 2110; Conservative
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1064	AGTGCGTGATGCTTATGGATTGTGGCTAGTATCTGTTATCTGCGAGGTCTGGTTTGCCTT 1123	ċ	0	E c
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1124	GICCIGGCITCTAGATCAGITCCCAAAATGGTATCCAATCAACCGTGAGACATATCTCGA 1183	a ë		CARAGAGAG
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1250	AGCTTCAATGCTGACTTTTGACGCTTGAGACTTCAGAGTTTGCTAGGAAATGGGT	Oy		TAAGTTGT
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1310) ACCATTIGIGAAGAAGTAIGAACCCAGAGCICCCGAGTITIACITIGCCAGAA 1369 	; d		CAGTTACG
1370		δy dq	2557	2446 ATTGCATG 2557 ACTGCATG
1484	NNTAGATTACCTGAAGGACAAAATTCAACCTTCATTTGTTAAGGAAAGACGCGCAATGAA 1543	ò	2506	TGAACCAA
1430) GAGAGAATATGAAGAATTTAAAATCAGGATAAATGCCCTAGTTTCTAAGGCATTGAAGT 1489 [1]	qq		 TTAATCAG
1490	GCCCGAGGAAGGATGATGCAAGATGGCACACCATGCCAGGAAACAATACCAGGA	Oy	2566	CCTTATGG
1604		ପ୍ର :		CTATCTGG
1550	TCATCCTGGAATGATTTCAGGTTTTCCTTGGTCACAGTGGTGGCCTTGATACTGAGGGTAA 1609	Z q	2737	CCATTGIT
1610	CCATCCTGGCATGATTCAGGGTGTTTTGGGGGCACAGTGGTGGGCTCCGGCATGGAAAAAAAA	Qy	2686	GTCTGCTC
1724		qa ,	2797	GTCTTCTT
1670	GAAGGCTGGTGCCATGAATGCCCTTGTTCGTGTCTCAGCTGTCCTTACTAATGGACAATA 1729 	ab ab	2857	TICCECTC
1730	CATGITGAATCTIGATGACACTACATCAACAACAACGCTGTCCGAGAAGCTAT 1	Q Q	2806	GCATTGAC
1844	TCTTCTCAATGTGGATTGCGACCATTACTTCAATAGCAGCAAAGCTCTTAGAGAAGCAAT	Qy	2866	TGTTTGC
1790	GRGTTGCTRATGGARGTCGAAACTTAGGTGCGCCAAGTTGGTGGTTTGGTGGTTTGGTGGTTGGT	qq	2977	TCTTCGCA
1850	GTTTGATGGGATTGATAGGAATGATCGATATGCAAACAGGAACACTGTCTTTTTGATAT 1909	oy Ob	3037	TCACCTCA TTACCTCA
1910	ATTIGATIGGCCTTGACTTGCACGATCGATGCTAATCGGAACATATGTTGTTTATTTTTTTT	ØΣ	2986	CGACGCTT
2024		ବୁଣ ବ	3097	CCAGTTTG
1970) CAACAGAACAGCTATCTATGGTTATGAGCCCCCAATTAAGGCGAAGAAGCCAGGTTTCTT 2029 	g qo		GAATTTCG
2030	GGCATCACTATGTGGGGGCAAGAAGAAGGCAAGCAAGTCAAAGAAAAGGAAGCTCAGATAA	oy G	3217	TCTTTGCC
214:	2143 ACATTGTTGAGGGCTGCNNNNNNNNNNNNNNNNNNNNNNN			

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TTGATGATGAGAAATCAGTTCTCATGTCTCAAA || ||||| | |||| || ||||| || || ACGAGGATGAAAGGTCAGTGCTTATGTCCCAGA FACCAATCATGGGGGCCGCTCTTTGGGAAGCTCT CTCCAATCTTCATTGCATCCACCTTTATGACTC CGCTTCTAGTCTATTGTATTGCCTGCTATCT CCCTTATCGCCTATTGTGTGCTTCCTGCTATCT CAGAGATTAGCAACTTGGCCAGTATCTGGTTCA AGTICIGGGICALIGGAGGIAICICIGCACAIC SAGTTTTGGGTTATTGGTGGCACCTCTGCCCATC GCGACTTTGCTGAGCTCTACATGTTCAAGTGGA **NTTTTGATCATTAACATGGTTGGTGTCGTTGCTG** CAGCAGCATTGTTGCCTCCACTCTGATGGAAT SAATGGGGAACTGAGATTGGTTGGATCTATGGAT TCAAGATGCACGCAAGAGGCTGGCGTTCAGTCT AGGGATCTGCCCCCATCAATCTTTCAGATCGTC GETTCTGTTGAAATTCTTTTCAGCCGGCATTGCC CTGGTATCCTTGAGATGAGGTGGAGTGGTTG AGGTGCTTGCCGGTATCGACACCAACTTCACTG CAGAATCTCTTTTGAAAGAAGCTATCCATGTCA CCTTCTGGGTGATTG || | | | | CCGTATTATGAAGA(TGGCTATGAGGACA TGGATATGAGGACA GCCCAAGCGCCCAG GTATGGCTACGGAG CACTGGAAAGTTCA TACCAATAAATTTA TTTCGCCTCCANNN CGTCTTTCAGGGTC AGTGTTCCAGGGTC AAAGGCTAATGACG AAAGGCATCTGATG CTACGCCATCAACA GGGTGTTGAAGGTG AGAGAAGAGATTTG GGAGAAACGCTTTG TGTTCCTCAGTCCT CATACCACCTTCAA AGAAGATATTCTTA |||| |GCCACCACGACCTT AGTGCTGCGGTGGG TTACCCACTAACCT TTATCCAATCACAT CTTCCTTTCAATTT CGAGTGGTGGAGGA TCTCATCCCTCCGA **PCGAACAAGCATGT**

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project" 2 others
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Malaley,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTCATTGTTCTGCGGTTGGTTGTTCTAAGCATCTTCCTGCACTACCGTCTCACAAATC
AAAACCGCACACGACGATTGTCATCGTCTGGGCTGTCCTCCTCGCTTCTATCTTCTCCT
          AGAACCGCACAACAATCGTCATTGTCTGGTCCATCTTCTTGCTTCTTCTCCCT
                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1320.4; DB 11; Length 2872; Pred. No. 0;
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/db_xref="MaizeDB:637064"
/db_xref="taxon:4577"
/clone="PCO121439"
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sequence.
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Zea mays PC0121439 mRNA
AY104236
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2 (bases 1 to 2872)
Coe, E.C.
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Matches 1760; Conservative
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144	TATGGTGGTGTTCCTCAGTCCTCCAGAATCTCTTTGAAAGAAGCTATCCATGTC 2324 	ataagtigtggctatgagacaagtctgaatggggaactgagattggttgg	TCTGTCACAGAAGATATTCTTACTGGATTCAAGATGCACGCAAGAGGCTGGCGTTCAGTC 2444 	TATIGCATGCCCAAGCGCCCAGCTITCAAGGATCTGCCCCCATCAATCTTTCAGATCGT 2504 	CTGAACCAAGTGCTGCGGTGGGCTCTCGGTTCTGTGAAATTCTTTTCAGCCGGCATTGC 2564 	CCCTTATGGTATGGCTACGGAGGGCCCTCAAGTTCCTGGAGAGATTCGCTTACATCAAC 2624 	ACCACCATTTACCCACTAACCTCTCCCGCTTCTAGTCTATTGTATATTGCCTGCTATC 2684 	TGTCTGCTCACTGGAAAGTTCATCATGGCAGATTAGCAACTTGGCCAGTATCTGGTTC 2744 	ATTGCGCTCTTCCTTTCATTTTCGCCACTGGTATCCTTGAGATGAGGTGGAGGGGGTGTT 2804 	GGCATTGACGAGTGGTGGAGGAATGAACAGTTCTGGGTCATTGGAGGTATCTCTGCACAT 2864 	CTGTTTGCGTCTTTCAGGTCTTCTGAAGGTGCTTGCCGGTATCGACAACTTCACT 2924 	GTCACCTCAAAGGCTAATGACGAAGAAGGCGACTTTGCTGAGCTCTACATGTTCAAGTGG 2984 	ACGACGCTTCTCATCCCTCCGACGACCATTTTGATCATTAACATGGTTGGT	GGCACCTCCTACGCCATCAACAGTGGTTACCAATCATGGGGGCCGCTCTTTGGGAAGCTC 3104 	TTCTTTGCCTTCTGGGTGATTGTTCACTTATACCCATTCCTCAAGGGTCTTATGGGCAGG 3164 	CAAAACCGCACCACGACGATGTCATCGTCTGGGCTGTCCTCCTCGTTCTATCTTCTCC 3224 	TTGCTGTGGGTTCGTGTTCACTACCCGT 3260
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HTC 25-MAY-2002 Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae; PACC pogoneae; Zea. thence is part of a project of EST ting from the application of public Dupont contigs; this resource was four as part of a collaboration for the g of BACs in conjunction with the Maize ao,G.H., Vogel,J.M., Whitsitt,M.S., Morgante,M. and Tingey,S.V. Ont Consensus Sequences for Design of CCAGATATGCGGCGACGAGGTCGGGGTGGGCTT 355 CGAGTGCGCCTTCCCCGTCTGCCGCGCCTGCTA 415 268 475 rggcactgaggaccagaagcagaagattgctga 385 CGGCGCGCGCGCGCGCCCGGACTTCAA 655 CCAGATCTGCGCCGACGGCCTGGGCACCACGTT 148 CGTCTGCCGCTTCCCGGTCTGCCGCCCTGCTA 208 GGAGGAAGGCGACGACTGATGCCGATGATGG 328 GGACGAGGAGGACGCGTCGACGACCTGGA 535 CGCCACGAGGACCACCGCAGTACGTCGCCGA 595 CGGGGGCAGTGCCAATGTTGGCCACCCCAAGTA 445 GTATGACAGTGGAGAGATCCCTAGGGGATACGT 505 CAACG-----GCCAGATGGTTGATG 702 AGGAGAAATCCCTGGAGCTTCGCCTGATCATCA 565 Gaps Maize Mapping Project, University of (211, USA e Mapping Project/DuPont Cornsensus GGCCTGCCTCCAGTGCAAGACCAAGTACAAGCG re 1319.8; DB 11; Length 3788; dd. No. 0; Mismatches 1030; Indels 103; 3 others linear = -mRNA 866 t ays" B:637005" 4577" 1788 bp ers Б Spermatophyta; Magna clade, Panicoideae; 1 (bases 1 to 3788) Hainey, C.F., Dolan, M Arthur, L.W., Hanafey Maize Mapping Projec Overgo Probes Unpublished (2002) 2 (bases 1 to 3788) overgo addr Mapping Pro a 954 c Location/ou 1. 3788 /organism= /db_xref="w /db_xref="th" /db_xref="th" /db_xref="th" /db_xref="th" /db_xref="th" /clone="this assemblies contigs to 36.4%; 296 CGCGCGCCGGGCGGAGGCG 506 CCCTTCAGTCACCAACAGCCAG 476 ccrcaaggrrgcccgcgggrg 536 GGGCGAGTTCGGCCTGCAGGAC 386 CAGGATGCGCAGCTGGCGCATG Submitted (25-APR-20 Missouri, Columbia, 149 GGACGCCGACGTCTTCACCGCC 356 CGACGGGAGCCCTTCGTGGCG 209 CGAGCACGAGCGCAAGGAGGGG 416 CGAGTACGAGCGCCGCGAGGG 269 CCACAGAGGGAGCCCAGCGATC 329 TAGTGACTTCAAC---TACCCT 596 grccardcreceeccecadare 446 TGACAGTGGCGAGATCGGCCTC 656 cccccarcccarccccarc Zea mays PC0120363 1 AY103701 AY103701.1 GI:21206 89 CGGGAGGCACGGGGCCGGGGAC Eukaryota; Viridipl assembled Query Match 36.4 Best Local Similarity 65.3 Matches 2129; Conservative Direct Submission Zea mays. Zea mays AY103701 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM source BASE COUNT ORIGIN REFERENCE AUTHORS REFERENCE AUTHORS JOURNAL JOURNAL AY 103701 FEATURES TITLE g à 셤 à ò g ò Ω δ Q οy g g

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Qy 2692 TCACTGGAAAGTTCATCATGCCAGAGATTAGCCACTTTCGCCAGTATCTGGTTCATTGCGC 2751	Oy 2872 CCGTCTTTCAGGGTCTTCTGAAGGTGCTTGCCGGTATCGACCAACTTCACTGTCACCT 2931	OY 2932 CAAAGGCTAATGACGAAGAAGGGGACTTTGCTGAGCTCTACATGTTCAAGTGGACGACGC 2991	QY 2992 TTCTCATCCTCCGACGACCATTTTGATCATTAACATGGTTGGT	QY 3052 CCTACGCCATCAACAGTGGGTTACCAATCATGGGGCCGCTCTTTGGGAAGCTCTTGT 3111	Qy 3112 CCTTCTGGGTGATTGTCACTTATACCCATTCCTCAAGGGTCTTATGGGCAGGCA	OY 3172 GCACACGACGATGTCATGGTCTGGCTGTCCTCGCTTCTATCTTCTCTTGCTGT 3231	QY 3232 GGGTTCGTGTTCATTCACTACCCGTCTCGCTGGCCCAAATATCCAAACTGTGGCA 3291	OY 3292 TCAACTGCTAGGAAGGGGGG 3313 	RESULT 7 AY104730 LOCUS AY104730 S783 bp mRNA linear HTC 25-MAY-2002 DEFINITION Zea mays PCO100501 mRNA sequence. ACCESSION AY104730		Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeee; Andropogoneae; Zea.	AUTHORS Hainey, C.F., Dolan, M., Mao, G.H., Vogel, J.M., Whitsitt, M.S., MITHORS Arthur, L.W., Hanefey, M., Morgante, M. and Tingey, S.V.	A.	Coe, E.C. Direct Submission	Missour	source 1. :3783 /organism="Zea mays" /db xref="MaizeDR:635765"	/db_xref="taxon:4577"

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٥	3134	ATACCCATTCCTCAAGGGTCTTATGGGCAGGCAAAACCGCACCGACGATGTCATCGT 3193	φ.	227	GGGCACCCP
q	3284	TTACCCGTTCCTCAAGGGTCTGGTTGGGAGGCAGAACAGGACGCCAACGATTGTCATTGT 3343	qa	383	GGGCACGCA
δλ	3194	CTGGGCTGTCCTCCTCGCTTCTTCTTCTTGCTGTGGGTTCGTGTTGATCCATTCAC 3253	QY	287	GATCCGCGG
q	3344	CTGGTCCATCCTCGCTTCGATCTTCTCGCTGCTTTGGGTCCGGATCGACCCGTTCCT 3403	qa	443	TGTGACCGG
δλ	3254	TACCCGTCTCGCTGGCCCAAATATCCAAACCTGTGGCATCAACTGCTAGGAAAGTGGGAG 3313	Qy	347	TGCATCTGG
ф	3404	тстесат	q _O	503	CGGCCATGA
δλ	3314	TTTGTAGA 3321	Qy	407	GAACACCGG
q	3464	CACGIGGA 3471	qa	551	GAGCTACGG
RESU	8		οy	467	CTCCAAGTA
AY103 LOCUS	AY103655 LOCUS	AX103655 3897 bp mRNA linear HTC 25-MAY-2002	q _Q	585	CCACAAGCT
DEFI	DEFINITION	Zea mays PC0096398 mRNA sequence.	Qy	527	GATGTCAGG
VERS	VERSION		qa	635	AATGGTGGA
SOURCE	URCE		QY	587	CATCAGCAG
			qС	695	GGGAAAGAG
PPPP	a DNG c	clade; Panicoldeae; Andropogoneae; Zea.	δλ	647	CTCCGGCAG
AU	AUTHORS	L (bases I to 302/) Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur F. W. Hanafar, M. Morranto M. and Mingon, C.V.	q	755	TATGGACCC
T	TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overco Drobes	Qy	707	GGACAAGGG
JOI	JOURNAL REFERENCE	Unpublished (2002) 2 (bases 1 to 3897)	qa	815	GATGGAGAA
AU	AUTHORS	Coe, E.C. Direct Submission	δλ	167	AGCTACTGA
ίĞ	JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia MC 65211 HGA	qa	875	TGATGATGG
FEAT	EATURES Source		δŏ	827	AACTCGCCA
	5		đ	914	AGCAAGACA
		/db_xref= taxpord577" /alaxed=taxpord577"	Qy	887	AATGGTCAT
		/clone- recognized // // // // // // // // // // // // //	qq	974	GATGATTAT
		/note"this sequence is part of a project of EST /note"this resulting from the analication of muching	Qy	947	TCCTGTGCG
		contigs to seed Dubont contigs, this resource was	q	1034	TCCGGTGAA
		overgo addressing of BACs in conjunction with the Maize	δŏ	1001	TTTATCCTG
BASE CO	BASE COUNT	982 a 839 c 1008 g 1068 t	qq	1094	CATGICITG
Quer) Best Matc)	Y Mo Loc	tch sal Similarity 63.9%; Score 1267.8; DB 11; Length 3897; 2108: Conservative 0: Mismarthes 1082: Indels 111. Gans 8.	Qy Dp	1067	TGATAGACT AGACCGGCT
Qy		CCCCCCCATGGACGCCGACGCGGACGCCCTGAAGTCCGGGAGGCACGGGGCCGG 106	δλ	1127	CATATTTGT
QQ	203 (අ .		TTTCTTGT
ογ	107	GGACGTGTGCCAGATCTGCGCCGACGGCTGGGCGTGGACGGCGGACGTCTTCAC 166	λ q _α	1187	1187 GCTATCCAT 1274 TCTATCTAT
g	263 (GCAGGTGTGCCAGATTTGCGGCGACGACGTCGGCCTTGCCCCCGGGGGGACCCCTTCGT 322	_	! !	

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7 CGGAGCTTCAATGCTGACTTTGACGCATTGGCTGAGACTTCAGAGTTTGCTAGGAAATG	7 GGTACCATTTGTGAAGAAGTATGAACCCAGAGCTCCGAGTTTTACTTTTGCCA	7 GAAAATTGATTACCTGAAAGACAAAGTCCAGCCTTCATTTGTTAAAGACCGCCGGGCCAT	7 GAAGAGAGAATTTGAAGAATTTAAAATCAGGATAAATGCCCTAGTTTCTAAGGCATTGAA 	7 AGTCCCCGAGGAAGGATGGATCATGCAAGATGGCACCACCATGGCCAGGAAACAATACCAG	7 GGATCATCCTGGAATGATTCAGGTTTTCCTTGGTCACGGGGGGGG	7 TAATGAGCTCCCCGGTTTAGTTTATGTGTCTCGTGAAAAGCGTCCTGGGTTCCAGCACCA	7 CAAGAAGCTGGTGCCATGAATGCCCTTGTTCGTGTCTCAGCTGTCCTTACTAATGGACA	7 ATACATGTIGAATCTIGATIGIGATCACCACCACAACAGCAAGGCTGTCCGAGAAGC	7 TATGIGCTICCTAATGGATCCAAACCTAGGTCGGAAGTCTGTTATGTGCAGTTCCCACA	7 PAGGITIGAIGGGATIGAIAGGAATGAIGGIATGCAAACAGGAACACTGICTTTTTIGA	7 TATTAACTIGAGGGCCTTGACGGCATTCAAGGACCAGITIATGIGGGAACTGGTIGTGT 	7 TITCAACAGAACAGCTATCTATGGTTATGAGCCCCCAATTAAGGCGAAGAAGCCA	2	O AAGCAAGTCAAAGAAAGGAGCTCAGATAAGAAAAAGTCGAACAAGCATGTGGA	4 CAGTICTGTICCAGTATICAAICTCGAAGACATAGAGGGGGGGTGTTGAAGGTGCTGGGTT	4 TGATGATGAGAAATCAGTTCTCATGTCTCAAATGAGCTTAGAGAAGAGATTTGGCCAGTC	4 AGCAGCATTTGTTGCCTCCACTCTGATGGAATATGGTGGTGTTCCTCAGTCCTCCACTCC	
1247	1307	1367	1427	1487	1547	1607	1667	1727	1787 1874	1847	1907	1967	2022	2060	2114	2174	2234	2294
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2647 2593 2707 2653 2767 2713 2827 2773 2887 2893 3007 3013 3073 3193 3304 3253 3313 3424 2467 3064 3184 2828 AGAGCTGAATAATGTTGCCAGCCTGTGGTTCATGTCACTTTTTATCTGCATATTTTGCTAC 2888 GAGCATCCTAGAAATGAGATGGAGTGGTGGTTGGAATTGATGACTGGAGGAGGAGGA GGTGCTTGCCGGTATCGACACCAACTTCACTGTCACCTCAAAGGCTAATGACGAAGAAGG 3125 GCTTCTATTGAACTTCATTGTGTGTGTCCTGGCGTTTCAAATGCGATCAATAACGGATA 3185 TGAGTCATGGGGCCCCCTCTTTGGAAGCTATTCTTTGCATTTTGGGTGATGTCCATCT TGCGAAGGATGATGGTCCGCTTCTTGAGGAGTGTGGTTTGGATTGCAACTAGGATGTCAG 2648 GTCTATTGAGATCTTCTTCAGCAATCATTGCCCTCTTTGGTATGGGTATGGTGGCGGTCT CCTCTTGGCTTACTGTACATTGCCTGCCATCTGTTTATTGACAGGGAAATTTATCACTCC AGAGATTAGCAACTTGGCCAGTATCTGGTTCATTGCGCTCTTCCTTTCAATTTTCGCCAC GITCTGGGTCATTGGAGGTATCTCTGCACATCTGTTTGCCGTCTTTCAGGGTCTTCTGAA 2954 CGACTTTGCTGAGCTCTACATGTTCAAGTGGACGACGCTTCTCATCCCTCCGACGACCAT 3014 TITGAICATTAACAIGGIIGGIGGTGTCGTIGCIGGCACCICCTACGCCATCAACAGIGGIIA CIGGGCTGTCCTCGCTTCTATCTTCTTCTTGCTGTGGGTTCGTGTTGATCCATTCAC 3254 TACCCGTCTCGCTGGCCCAAATATCCAAACCTGTGGCATCAACTGCTAGGAAAGTGGGAG CAAGATGCACGCAAGAGGCTGGCGTTCAGTCTATTGCATGCCCAAGCGCCCCAGCTTTCAA GGGATCTGCCCCCCATCATCTTTCAGATCGTCTGAACCAAGTGCTGCGGTGGGCTCTCGG 2534 ITCTGTTGAAATTCTTTTCAGCCGGCATTGCCCCTTATGGTATGGCTACGGAGGGGGCGCT CAAGITCCIGGAGAGAITCGCTTACAICAACACCACCAITTACCCACTAACCICTCCC GCTTCTAGTCTATTGTATATTGCCTGCTATCTGTCTGCTCACTGGAAAGTTCATGTCC TGGTATCCTTGAGATGAGGTGGAGTGGTGTTGGCATTGACGAGTGGTGGAATGAACA CCAATCATGGGGGCCGCTCTTTGGGAAGCTCTTCTTTGCCTTCTGGGTGATTGTTCACTT 3134 ATACCCATTCCTCAAGGGTCTTATGGGCAGGCAAAACCGCACACCGACGATTGTCATCGT 3425 T 3314 - E-1 2408 2414 2528 2474 2594 2708 2654 2768 2714 2774 2834 2894 3008 3074 3194 3305 3314 3425 염 qq Qy Db 07 07 08 OY Db Ω Qy Db OY Db OY Db 0y Db 0y g QY Db δy qq δŽ 임 QΥ g QΫ́ g g Qγ QΥ

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RESULT

CATTGGA CTCTGCCCAT 			916 bp AF200526 11ulose synthase-: a maysl, (Alellose catannamed pr	GI:1915; are. are 'inidiple ; Streptopl 'a, Magne hyta; Lille	0 8 0		/strain="c" bk" /strain="c" bk" /db_xref="c" 4513" /clone="HC] 9_T3.abl" /clone=lib /tissue_typ /dev_stage* /note="6 ap hour droug moist paper by rel. hum 209 c g 272
Db 407 GAACAGTTCTGGGTCATTGGA QY 2889 CTGAAGGTGCTTGCCGGTATC Db 467 CTGAAGGTGCTTGCCGGTATC QY 2949 GAAGGCGACTTTGCTGAGCTC QY 2949 GAAGGCGACTTTGCTGAGCTC QY 3009 ACCATTTGATCATTAACATG Db 527 GAAGGCGACTTTGTTAACATG	9 3069 GGTTACCAATGGGGGGCCGG	3189 767 3248 827	RESULT 10 BM816139 LOCUS DEFINITION HC105609_T3.abl HC 1 similar to (AF200528 cellulose synthase- [Zea mays], cellulos thallana], unnamed pr	ACCESSION BM816139 GI:1915. VERSION BM816139.1 GI:1915. KEYWORDS EST HOrdeum vulgare. ORGANISM Hordeum vulgare. Eukaryota viridipli. Spermatophyta; Magnil		COMMENT CONTACT: Mark A. Fr Plant Biology University of Illing 1201 W Gregory Dr. Tel: 2172655473 FEATURES Email: bohnertlab@il. Source I. 1916	/orga /stra /db_x /db_x /clon /tlos /dev_ /note BASE COUNT 212 a 2
	Track Including to () The contract of the con		u o	5;	2528 106 2588 166	2648 226 2708 286	27.08 34.6 28.28 28.88
BM816138 HC109B12_T3.abl HC Hordeum vulgare CDNA clone HC109B12_T3.abl similar to (AF200528) cellulose synthase-4 [Zea mays], (AF200529) cellulose synthase-5 [Zea mays], (AF200533) cellulose synthase-9 [Zea mays], cellulose synthase catalytic subunit [Arabidopsis Haliana], unnamed protein product [Arabidopsis thaliana], mRNA sequence. BM816138 HG19152152 Hordeum vulgare. Hordeum vulgare.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeau; Triticeae; Hordeum. ; Triticeae; Hordeum.] (bases 1 to 80 M. Ozturk, N. Z., Michalowski, C. B., Brazille, S., Borchert, C., Palacio, C., Normand, C., Murphy, C., Kelley, R., Sant, S.A., McLaughlin, H., Fredricksen, M.A. and Bohnert, H., T., Mornand, C., Murphy, C., Relley, R., Sant, S.A., McLaughlin, H., Monitoring large-scale changes in transcript abundance in drought-	and salt-stressed barley Unpublished (2002) Contact: Mark A. Fredricksen Plant Biology University of Illinois 1201 W Gregory Dr. Urbana, IL 61801, USA Tel: 2172655473 Email: boinertlab@life.uiuc.edu.	1880 /organism="Hordeum vulgare" /organism="Hordeum vulgare" /organism="Texton: 4513" /clone="HC109B12_T3.ab1" /clone="HC109B12_T3.ab1" /clone="texton: 4513" /clone="texto	166 a 240 c 21.0%; Similarity 96.2%; 1; Conservative (TTCAAGGATCTGCCCCCATCAATCTTTCAGATCGTCTGAACCAAGTGCTGCGGGGGGGCTTT 1 1 1 1 1 1 1 1 1	CGCCTCAAGTTCCTGGAGAGATTCGCTTACATCAACACCACCATTTACCCACTAACCTCT [AIGCCAGAGATTAGCARCITAGCAGAGATTAGCAGAGATTAGCAGAGAGAGAGAGAGAG
BM816138 LOCUS DEFINITION VERSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	AL.	source	SE COUNTIGIN Ouery Me Best Loc Matches	Qy 2469 TT Db 48 TT Qy 2529 CT Db 107 CT	Oy 2589 CG Db 167 CG Oy 2649 CT Db 227 CT Oy 2709 ET	287 287 2769 347 2829

mRNA linear EST 05-MAR-2002 re cDNA clone HC105G09_T3.abl synthase-4 [Zea mays], (AF200529) (AF200533) cellulose synthase-9 ealytic subunit [Arabidopsis t [Arabidopsis thallana], mRNA phyta; Embryophyta; Tracheophyta; lopsida; Poales; Poaceae; Pooldeae razille,S., Borchert,C., Palacio,C.
R., Sant,S.A., McLaughlin,H., transcript abundance in droughtuught stress by placing plants on imidity) in light" 2 t GACGACGCTTCTCATCCCTCCGACG 3008 CCTTCTTGCCTTCTGGGTGATGTT 3128 GGCAAAACCGCACACGACGATTGTC 3188 TGGCACCTCCTACGCCATCAACAGT 3068 CTTGCTGTGGGTTCGTGT-TGATCC 3247 TCTGTTTGCCGTCTTTCAGGGTCTT 466 ACCTGTGGCATCAACTGCT 3300 101, USA are"

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/Lissue_type="Vernalized apex"
/dev.stage="One month old plants"
/dev.stage="One month old plants"
/dev.stage="Coni XLOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: ECORI; Site_2: Xhoi; One-month old plants were
subjected to vernalization treatment by placing them in
the cold room at 6. under 15hr light/9hr dark condition.
Total RNA was prepared from apex tissue extracted from
plants with no cold treatment; and from plants with 2-week
/ 4-week and 6-week cold treatment separately. Equul
amount of total RNA was pooled from all four samples, a
cDNA library was made using pooled polyA RNA and cDNA
clones were in vivo excised at the University of
California, Davis (V. Echenique, B. Stamova, J. Dubcovsky
). Plasmid DNA preparations and DNA sequencing were
performed in the Ob Anderson lab (all other authors)."
                                               Triticum monococcum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Doales; Poaceae; Pooideae;
Triticeae; Triticum.
1 (bases I to 762)
Anderson, O.D., Chao, S., Crossman, C., Dubcovsky, J., Echenique, V.,
Lazo, G.R., Pham, J., Rausch, C.J., Stamova, B., Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
genomes - Vernalized apex cDNA library from Triticum monococcum
Unpublished (2002)
                                                                                                                                                                                                                                         Contact: Olln Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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/clone="WHE2829_H06_O11"
/clone_lib="Triticum monococcum vernalized apex cDNA
library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.7%; Score 750.4; DB 14; Length 762; Best Local Similarity 99.9%; Pred. No. 2.1e-198; Matches 751; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                               Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
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                                   Length
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OY 925 TCCTGCACTACCGTCTCACAAATCCTGTGCGTAATGCCATACCCACTGTGGCTTTAATCTG 984	Db 491 CGTCTCAGTTGGCTGTTGACATATTTGTCAGTACAGTCGACCCCTTGAAGGACCAC 550 Qy 1165 CTATCGTCACTGCCAACACTGTGCTTCCATTCTTGCTGTTGATTATCCCGTGGACAAGG 1224 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 1225 TCTCTTGCTATGTATCTGATGACGGAGCTTCAATGCTGACTTTTGACGCATTGGCTGAGA 1284		Db 731 CTCCCGAGTTTTACTTTTGCCAGAAATTGAT 762	MESULT 1.2 BG368813 LOCUS BG368813 LOCUS BG368813 BG368813 BG368813 BG70 bp mRNA linear EST 22-OCT-2001 DEFINITION HYSME10020M13f Hordeum vulgare 20 DAP spike EST library HYSDNA0010 (20 DAP) Hordeum vulgare CDNA Clone HYSME10020M13f mRNA sequence.	NOI NOI SC	SOURCE Hordeum vulgare. ORGANISM Hordeum vulgare ORGANISM Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae	REFERENCE 1 (bases 1 to 870) AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu, Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton	AL	COMMENT COLLECT: Wing KA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA	fer: 864 656 4293 Fax: 864 656 4293 Email: rwing@clemson.edu Total hq bases = 537 Seq primer: AATTAACCCTAAAAGG	High quality sequence stop: 777. FEATURES Location/Qualifiers source 1.870		/Clone_lib-"Hordeum vulgare 20 DAP spike EST library HYCDNA0010 (20 DAP)" /tissue_type="20 DAP spike"

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perpared, poly(A) RNA was purified, one led CDNA library was made, and 1 million excised to give palluescript SK(-) CDNA TJ Close lab at the University of ariolace in the University of erside (Choi). Phagemids were plated and lemson University Genomics Institute (CUGI) Frisch, Atkins and Wing). Plasmid DNA NA sequencing and sequence analysis were sil (Wing, Yu, Frisch, Henry, Simmons, Oates The sequence has been trimmed to remove and contains a minimum of 100 bases of a rabove. For more details on library sequence analysis see he.clemson.edu/projects/barley. To order itp://www.genome.clamson.edu/orders Also ng K. Kleinhoffs A. Wise R (2001) physically anchored EST resources for Barley Genetics Newsletter 31:29-30.

* usda.gov/gpages/Dgn/31/cover.html)"

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lambda2AP; Site_1: EcoR1; Site_2: Xhol;
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/clone=ib="Wheat unstressed seedling shoot cDNA library"
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/lab_host="E. coll SOLR"
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/site_l: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
/germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Shoots were
harvested. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the CDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Choi, Close, Fenton) at the University of
Callifornia, Riverside: Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab (all
other authors)."
                                                                                                                                                                                                                                                                                                                                             T67 bp mRNA linear EST 19-JUN-2002 WHE0309_E10_I192S Wheat unstressed seedling shoot cDNA library Triticum aestivum cDNA clone WHE0309_E10_I19, mRNA sequence. B0578769 G1:21482086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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1 (bases 1 to 767)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes · Etiolated shoot cDNA library
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Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
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Dread wheat.
Triticum aestivum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
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                                                                                              CCGATGCCGATGATGCCAGTGACTTCAACTACCCTGCATCTGGCACTGAGGACCAGAAGC
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                                      Indels
Score 689.6; DB 14
Pred. No. 2.3e-181;
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0; Mismatches
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2938 372 2998 432 3058 3118	Db 552 GGGTGATTGTTCACTTATAC Qy 3178 CGACGATTGTCATCGTCTGG Db 612 CGACGATTGTCATCGTCTGG Qy 3238 GTGTTGATCCATTCACTCTGG Qy 3238 GTGTTGATCCATTCACTACC Db 672 GTGTTGATCCATTCACTACC RESULT 15 BF624748 LOCUS BF624748 BF624748 DFFINITION HYSMEAO017K05f HORN HYCDNAA0001 (COLd s MRNA sequence. ACCESSION BF624748.2 GI:130 KEYWORDS SOURCE HORGHUM VULGATE CORGANISM HORGHUM VULGATE SOURCE EURATYOTA; VITIGID SPETERENCE 1 (bases 1 to 750 AUTHORS WING, R., T. J.	TITLE Development of a green for beneficially and long library genomic library genomic library genomic longulished (2001) COMMENT On Dec 18, 2000 th Contact: Wing RA Contact: W	Tel:son university Tel: 864 656 7288 Fax: 864 656 4293 Fax: 864 656 4293 Fox: 864 6	/organism /cultivar /db_xref= /clone="H /clone="H /rissue_t/ /lab_most /note="ver /note="ver Seeds wer condition
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han , P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. TITLE The structure and function of the expressed portion of the wheat genomes - Normalized shoot cDNA library JOURNAL Unpublished (2000) COMMENT Unpublished (2000) COMMENT Ontact: Ollh Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 510559573 Fax: 510559573 Fax: 510595818 Email: candersn@pw.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20	Seq primer: Seq primer: Location/Qualifiers 1710	BASE COUNT 139 a 189 c 166 g 216 t ONEGIN Query Match Best Local Similarity 99.1%; Pred. No. 2.56-181; Matches 693; Conservative 0; Mismatches 6; Indels 0; Gaps 0; OY 2578 GCTAGGAGGGGGCGCTCAAGTTCCTGGTTACATCAACACCACCATTTACC 2637	12 GETACGGAGGGGCCTCAAGTTCGTTACTTTTTTTTTTCCTTTTTTCCTTTTTTCCTTTTTTCCTTTT	Oy 2758 TTTCAATTTCGCCACTGGTATCCTTGAGATGGGTGGAGTGGTGTTGGCATTGACGAGT 2817 192 TTTCAATTTTCGCCACTGGTATCCTTGAGATGAGGTGGAGTGGTGTTGCCATTGACGAGT 2817 193 TTTCAATTTTCGCCACTGGTATCCTTGAGATGAGGTGGTGTTGCCATTGACGAGT 251 Qy 2818 GGTGGAGGAATGAACAGTTCTGGGTCATTGAGGTATCTTGCCACTTTGCCGTCT 2877

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750 bp mRNA linear EST 17-OCT-2001 sigare seedling shoot EST library Hordeum vulgare cDNA clone HVSMEa0017K05f,
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ayta; Liliopsida; Poales; Poaceae; Pooldeae
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ice sterilized then germinated under axenic
te dark at room temperature on filter paper
atth and cefotaxime in covered
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Rambo, T., Simmons, J., Oates, R., Choi, D.W.
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SAGCTCTACATGTTCAAGTGGACGACGCTTCTCA 2997
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          TCCTCGCTTCTATCTTCTCTTGCTGTGGGTTC 3237
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crystallization dishes. Five-day old seedlings were incubated at 50c for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University and Wing). Plasmid DNA preparations balmer, Frisch, Atkins and Wing). Plasmid DNA preparations, UNI sequence and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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212

BASE COUNT ORIGIN

2018 2078 CAGCACCACAAGAAGGCTGGTGCCATGAATGCCCTTGTTCGTGTCTCAGCTGTCCTTACT 1718 1719 AATGGACAATACATGTTGAATCTTGATTGTGATCACTACATCAACAACAGGCTGTC 1778 CGAGAAGCTATGTGCTTCCTAATGGATCCAAACCTAGGTCCGCAAGTCTGTTATGTGCAG 1838 TITITIGATATIAACTIGAGGGCCTIGACGGCATICAAGGACCAGITTATGIGGGAACT 1958 ACTGAGGGTAATGAGCTCCCCCGTTTAGTTTATGTGTCTCGTGAAAAGCGTCCTGGGTTC 1658 1479 GCATTGAAAGTCCCCGAGGAAGGATGGATCATGCAAGATGGCACCCATGGCCAGGAAAC 1538 300 009 240 AATACCAGGGATCACCCTGGAATGATTCAGGTTTTCCTTGGTCACAGTGGTGGCCTTGAT 120 Gaps 9 GGTTGTGTTTTCAACAGAACAGCTATCTATGGTTATGAGCCCCCCAATTAAGGCGAAGAAG AATACCAGGGATCATCCTGGAATGATTCAGGTTTTCCTTGGTCACAGTGGTGGCCTTGAT 241 AATGGACAATACATGTTGAATCTTGATTGTGATCACTACATCAACAACAACAGCAGGCTGTC ä 19.0%; Score 687.8; DB 12; Length 750; ilarity 95.6%; Pred. No. 7.2e-181; Conservative 0; Mismatches 32; Indels 1; Local Similarity nes 718; Conserv Query Match Matches 1539 1599 1659 1779 1839 1899 1959 2019 19 181 481 541 g g ò 9 δ g g 8 δŻ g ò ŏ g g ò ò g ŏ ò

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1: /cgn2_6/ptodate/1/lna/5A_COMB.seq:*
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6: /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Gaps

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DB 4; Length 3328; Indels Query Match 33.5%; Score 1215.6; DB 4; Best Local Similarity 69.2%; Pred. No. 0; Matches 1710; Conservative 0; Mismatches 739;

; OTHER INFORMATION: Synthetic Oligonucleotide US-08-960-048-1

927 CTGCACTACCGTCTCACAAATCCTGTGCGTAATGCATACCACTGTGGGCTTTTATCTGTT 986

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Description	Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli	Sequence 167, App
SUMMARIES	US-08-960-048-1 US-07-951-715A-6 US-08-459-595A-6 US-08-459-595A-6 US-08-459-544-6 US-09-053-549-7 US-09-053-549-7 US-09-053-549-7 US-09-103-549-7 US-08-258-261B-6 US-08-258-261B-6 US-08-258-261B-6 US-08-457-342-6 US-08-457-342-6 US-08-457-342-6 US-08-457-343A-4 US-08-457-333A-4 US-08-66-048-2 US-08-729-214-6 US-08-729-214-6 US-08-729-214-6 US-08-78-214-6 US	-09-056
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1047 ATCAACCGGGAGACCTACCTTGATAGACTGGCTTTAAGGTATGACCGAGAAGGTGAACCG 1106

857 GITAACAGGGAAACATACATIGACAGACTATCIGCAAGATAIGAAAGAGAAGGIGAACCI 916

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	34		Н	1452	4	US-09-726-651A-5	'n
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	4	44	1.2		4	US-09-105-537-7	7,7
O	4	44	1.2	5970	m	US-09-320-878-21	Sequence 21, Appl
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٠.	GEN	GENERAL INFORMATION:	RMATION				
. ••	AP	APPLICANT:	Stalker,		al		
. ••	H	TITLE OF INVENTION:	VENTION		Se	Plant Cellulose Synthase and Pro	Promoter
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•	S	RRENT APPI	LICATIO	N NUMBER	5	CURRENT APPLICATION NUMBER: US/08/960,048C	
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Qy	2247		IGTICCICAGICCICCACICCAGAAICTCTIIG 2306
qa	2042	GAATCTACACT	
Qy	2307	AAAGAAGCTATCCATGTCATA	TGGCTATGAGGACAAGTCTGAATGGGGAACTGAG 2366
qa	2102		rgcctatgaagactgcatggggaaagag 2161
δō	2367	ATTGGTTGGATCTATGGATCT	AGAGGATATTCTACTGGATTCAAGATGCACGCA 2426
qa	2162	ATTGGATGGATATATGGTT	reaccaraterraaccecricaaaarceacrec 2221
Qy	2427	AGAGGCTGGCGTTCAGTCTATT	SCCCAAGCGCCCAGCTTCAAGGATCTGCCCCC 2486
qa	2222	O	SCCTTAAGGCCAGCATTCAAAGGATCTGCACCC 2281
Qy	2487	ATCAATCTTTCAGATCGTCTG	AGTGCTGCGGTGGGCTCTCGGTTCTGTTGAAATT 2546
qa	2282		SCTTCTTCGATGGCTCTTGGATCTCTTGAATT 2341
Qy	2547	5 -	STATGGCTACGGAGGGCGCCTCAAGTICCIG 2603
qa	2342	Trccradcaggarrec	STATEGETTTEGAGGTEGTETTAAATGGETT 2401
QY	2604	GAGAGATTCGCTTACATCAACA	CATTTACCCACTAACCTCTCCCGCTTCTAGTC 2663
qq	2402	O	TGTCTATCCTTTCACATCCCTTCCACTCATTGCC 2461
Qy	2664	TATTGTATATTGCCTGCTATCT	SCTCACTGGAAAGTTCATCATGCCAGAGATTAGC 2723
qa	2462	- E-	CTCACAGGAAATTTATCATACCAACGCTCTCA 2521
δλ	2724	AACTTGGCCAGTATCTGGTTCA	SCICITCCTITCAATITTCGCCACTGGTATCCTT 2783
qq	2522		CTTTTCCTTTCCATTATCGTGACTGCTGTTTCTC 2581
Qγ	2784	GAGATGAGGTGGAGTGTTG	GACGAGTGGTGGAGGAATGAACAGTTCTGGGTC 2843
qα	2582	GAGCTCCGATGGAGTGGTGTCA	GAGGACTTATGGCGTAACGAGCAGTTTTGGGTC 2641
QY	2844	ATTGGAGGTATCTCTGCACATC	GCCGTCTTTCAGGGTCTTCTGAAGGTGCTTGCC 2903
qa	2642		GCCGTCTTCCAAGGTTCCTTAAGATGCTTGCG 2701
QY	2904	GGTATCGACACCAACTTCACTG	TCAAAGGCTAATGACGAAGAAGGCGACTTTGCT 2963
qq	2702	GGCATTGACACCAACTTTACTG	cccaaadcacridardardcaGariricgr 2758
ΟY	2964	GAGCTCTACATGTTCAAGTGGA	CITCTCATCCTCCGACGACCATTTTGATCATT 3023
qq	2759	GAGCTCTACATTGTGAAATGGA	CTTCTAATCCTCCAACAACACTCCTCATCGTC 2818
Qy	3024	AACATGGTTGGTGTCGTTGCTG	TCCTACGCCATCAACAGTGGTTACCAATCATGG 3083
qq	2819	AACATGGTTGGTGTTGCCG	rccardccrcadaadggraccaagcrrcg 2878
Qy	3084	GGGCCGCTCTTTGGGAAGCTCT	GCCTTCTGGGTGATTGTTCACTTATACCCATTC 3143
QQ	2879	GGACCACTCTTTGGCAAAGTGT	TCCTTCTGGGTCATCTCTTTATCCATTC 2938
Qy	3144	CTCAAGGGTCTTATGGGCAGGG	CGCACACCGACGATTGTCATCGTCTGGGCTGTC 3203
QO	2939	crcanagercrrargegaceco	AGGACACCATGTTGTCTTTGGTCAGTG 2998
Qy	3204	CICCICGCIICIAICIICICICI	FEGETTCETGTTGATCCATTCACTACCCGTCTC 3263
QQ	2999	rigrigecricistrations	recerrecareaceerrrereacecee 3058
ΟŻ	3264	GCTGGCCCAA 3273	
QO	3059	GATAGCACCA 3068	

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3390 CACCGCCAGCTGAACTACAAGCCCACCTACGAGGAGGAGCAACCTACACCGGACGTGCGCGG 3449
                                                                   3213 CCACGAGATCGAGAACAACACCGACGAGCTGAAGTTCAAGAACCGCGAGGAGGAGGAGGT 3272
                                        113 GIGCCAGATCTGCGCCGACGGCCTGGGCACCACGTTGGACGGCGACGTCTTCACCGCCTG 172
                                                                                                                        233 CCAGGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGCCACAGAGAGCCCAGCGATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: No. 5859336artls Corporation
The Brent & Trademark Dept., 520 White Plains
Red. PoB 2005
Tracrytown
New York
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN 1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMUNICATION INFORMATION:
TELEFRONE: (919)541-8689
TELEFRAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25.5EP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
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Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
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Desai, Nalini M.
Lewis, Kelly S.
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Warren, Gregory W.
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Dawson, John L.
Dunder, Erik M.
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US-08-459-448A-6
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TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.6%; Score 59; DB 1; Length 3624; Best Local Similarity 54.4%; Pred. No. 6.6e-06; Matches 141; Conservative 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PAtentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Full-length, maize optmized cryIB" /note= "Disclosed in Figure 6."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REFRENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEPHONE: (919)541-8669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
                                 Sequence 6, Application US/07951715A Patent No. 5625136 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
Pace, Gary M.
                                                                                              Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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: LOCATION: 1..3621
: OTHER INFORMATION: CTHER INFORMATION: CTHER INFORMATION: CTHER INFORMATION: US-07-951-715A-6
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STATE: New York
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                            Length 3624;
                                                                                                                                                                                                                                                                                           1.6%; Score 59; DB 2; Length 362
54.4%; Pred. No. 6.6e-06;
Live 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
STREET: Tarrytown
STREET: New York
                                                                                                                                                                                                     /product= "Full-length, maize optmized cryIB" /note= "Disclosed in Figure 6."
                                                                                   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
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Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
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Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
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Warren, Gregory W.
Evola, Stephen V.
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Lewis, Kelly S.
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            SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
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                                                                                                                                                                                                                                                                                                                           Matches 141; Conservative
                                                                   STRANDEDNESS: single
                                                                                                                                                                                       LOCATION: 1..3621
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                    nucleic acid
                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                      HYPOTHETICAL: NO FEATURE:
                                                                                                                                                                        NAME/KEY: CDS
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INFORMATION FOR
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US-08-459-595A-6
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SCAACGACTACACCGCCCACCAGGGCACCGCCGG 3329
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Isclosed in Figure 6."
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1.0, Version #1.30
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tic DNA"
                                                                                                                                              , 595A
                                                                                                                                                                                                                                                                                                                      2,027
                                                                                                                                                                                  CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US

FILING DATE: 25-SEP-199:

PRIOR APPLICATION NUMBER: US

FILING DATE: 04-02T-199:

ATTORNEY/AGENT INFORMATION

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40-

REFERENCE/CDCCKET NUMBER: 7-

TELECOMMUNICATION INFORMATI

TELEPHONE: (919)541-8689

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

SEQUENCE AND SEG DAIRS

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGIE
                  MEDIUM TYPE: Floppy dis
COMPUTER: IBM PC COMPAL
OPERATING SYSTEM: PC-DO
                                                                                       SOFTWARE: PATENT: TO SOFTWARE: PATENT: CORRENT APPLICATION DATA: APPLICATION UNBER: US/FILING DATE: 02-JUN-1991 CLASSIFICATION: 800
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optm
/not
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Patent No. 6075185
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APPLICANT: Koziel, Michae
APPLICANT: Bozal, Nalini
APPLICANT: Lewis, Kelly S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 54.4
Matches 141; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: , OTHER INFORMATION: , OTHER INFORMATION: O , OTHER INFORMATION: // US-08-459-595A-6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
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ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
3330 crececceacecrecaacaececcaaceccecaacecraceaececraceaececraceaecac 3389
                                                                                                                                                                                                        3390 cacceccaecergaacracaaecccaccraceaegaggaggaccracacccacerecece 3449
                                                                                                                                                             233 CCAGGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGCCACAGAGGGAGCCCAGCGATCCG 292
                                                                     CGACGTCTGCCGCTTCCCGGTCTGCCGCCCTGCTACGAGCACGAGGGCAAGGAGGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Launis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED NUCLEIC ACID CODING SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8687
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08459444A Patent No. 6121014 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Koziel, Michael G. Desai, Nalini M. Lewis, Kelly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
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ZIP: 27709
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO
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US-08-459-444-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                      APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 59; DB 3; Length 3624; 54.4%; Pred. No. 6.6e-06; ive 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Full-length, maize optmized cryIB" /note= "Disclosed in Figure 6."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/459,595
FILING DATE: 02-JUN-1995
FILING DATE: 25-SEP-1992
PRIOR APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
RECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEPHONE: (919)541-8587
TELEPHONE: (919)541-8587
TELEPHONE: (919)541-8587
TELEPHONE: (919)541-8589
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARRACTERISTICS:
TENDERAY: 0.01046, acid base pairs
                                                                                                                                                                                                                                                                                                                                                STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: NG COUNTRY: USA ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             Rothstein, Steven J.
Bowman, Cindy G.
Dawson, John L.
Dunder, Erik M.
                                                                  Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
                       Warren, Gregory W. Evola, Stephen V.
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Best Local Similarity 54.4<sup>1</sup>
Matches 141; Conservative
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EDNESS: single
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OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS:
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APPLICANT:
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APPLICANT:
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NAME/KEY:
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                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                        3330 CTGCGCCGACGCCTGCAACAGCCGCAACGCCGGCTACGAGGACGCCTACGAGGTGGACAC 3389
                                                                                                                                                                                                                                                                                                                                                                                              173 CGACGTCTGCCGCTTCCCGGTCTGCCGCCCTGCTACGAGCACGAGGAGGGGCAC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 CCAGGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGCCACAGAGGGAGCCCAGGGATCCG 292
                                                                                                                                                                                                                                53 CCGCGCCATGGACGCCGACGCGCCCTGAAGTCCGGGAGGCACGGGGCCGGGGACGT 112
                                                                                                                                                                                                                                                                                                                113 GTGCCAGATCTGCGCCGACGCCTTGGACGTTGGACGCGACGTCTTCACCGCTG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Desai, Nalini
TITLE OF INVENTION: No. 6121521el Insecticidal Protein and Gene
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6121521artis Corporation
                                                                                                                                              1.6%; Score 59; DB 3; Length 3624;
54.4%; Pred. No. 6.6e-06;
iive 0; Mismatches 115; Indels
LOCATION: 1..3621
OTHER INFORMATION: /product= "Full-length, maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                         optmized cryIB"
/note= "Disclosed in Figure 6."
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/053,549 FILING DATE: 01-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGC 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-053-549-7
US-09-053-549-7
Sequence 7, Application US/09053549
Patent No. 6121521
GENERAL INFORMATION:
APPLICANT: Desai, Nalini
APPLICANT: Desai, Nalini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFRENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3054 Cornwallis Rd. CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 CGGGGAGGAAGGCGACGAC 311
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EDNESS: single
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                                                                                                                                                                    Local Similarity
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HYPOTHETICAL:
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                                                                                                                                                Query Match
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                                                                                                                                                                              CACCACGTTGGACGCCACGTCTTCACCGCCTG 172
                                                                                                                                                             CCTGAAGTCCGGGAGGCACGGGGCCGGGGACGT 112
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                        CCCTGCTACGAGCACGAGCGCAAGGAGGGCAC
                                                                                                                                                                                                                                                                                                                                                     GTACAAGCGCCACAGAGGGAGCCCAGCGATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C DNA SEQUENCE HAVING ENHANCED IDAL ACTIVITY IN MAIZE
                                                                                              DB 3; Length 3624;
                                                                                            re 59; DB 3; Length 362
id. No. 6.6e-06;
Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ase #1.0, Version #1.30
                                                sclosed in Figure 6."
                "Full-length, maize rylB"
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APPLICATION NUMBEF
FILING DATE: 25-SF
APPLICATION NUMBEF
FILING DATE: 04-OC
                                                                                            1.68
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                                                                                                                                                             53 CCGCGCCATGGACGGCGACGCG
                                                                                                                                                                               3330 crececceacecrecaacae
                                                                                                                                                                                                                                                                                                                                                                                                                   293 CGGGGAGGAAGGCGACGAC 31
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Patent No. 6320100
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3054 Cornv
CITY: Research Tri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC of OPERATING SYSTEM: SOFTWARE: Patentin
                                                                                                                                                                                                                           113 GIGCCAGAICTGCGCCGACGG
                                                                                                                                                                                                                                                        3273 GTACC --- CCACCGACACCGG
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                                                                                                                                                                                                                                                                                                                                                     233 CCAGGCCTGCCTCCAGTGCAAC
                                                                                                                                                                                                                                                                                                                                                                                     3390 CACCGCCAGCGTGAACTACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Koziel, Mic
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Evola, Stepi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kramer, Van
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Merlin, Ell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crossland,
                                                                                                                               Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: NO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis,
LOCATION: 1.3621
CTHER INFORMATION:
OTHER INFORMATION:
CTHER INFORMATION:
US-09-053-549-7
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                                                                                                               Best Local Similarity
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TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                             Query Match
Best Local Similarity 48.69
Matches 152; Conservative
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CLASSIFICATION: 435
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COUNTRY: USA
ZIP: 22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-232-463-14
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APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Tuerk, Craig
APPLICANT: Tuerk, Craig
TAPLICANT: Fillow, Darathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEXOZ/C1-Con
FILE REFERENCE: NEXOZ/C1-Con
CURRENT APPLICATION NUMBER: 07/829,461
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 1991-08-01
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3624;
                                                                                                                                                                                                                                                                                                                                                                                         /product= "Full-length, maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 54.4%; Score 59; DB 4; Length 362 Similarity 54.4%; Pred. No. 6.6e-06; Conservative 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                        DESCRIPTION: /desc = "Synthetic DNA"
                 NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Disclosed in Figure 6.
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3624 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09197649 Patent No. 6194550
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                   optmized cryIB"
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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LENGTH: 390
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115 GCCAGATCTGCGCCGACGGCCTGGGCACCACGTTGGACGGCGACGTCTTCACCGCCTGCG 174
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                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                       55 GCGCCATGGACGGCGACGCCCTGAAGTCCGGGAGGCACGGGGCCGGGACGTGT 114
                                                                                                                                                                                                                                                                                  FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: Sequence;
COTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
COTHER INFORMATION: fragments having NCOI restriction sites.
US-09-197-649-7
                                                                                                                                                      Length 390;
                                                                                                                                                   1.5%; Score 55.4; DB 4; Length 3
48.6%; Pred. No. 1.8e-05;
tive 0; Mismatches 161; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CIPY: Alexandria
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ER: 30472/114 IMMU
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ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 I
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APPLICATION NUMBER: US/07/935,313
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CICGAGCGGATCGGCGACGCCTCGCCCGGAGA 24645
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Mismatches 106; Indels 0;
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.0, Version #1.25
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                                                                                                                                                                                                                                                                                                           NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATI
TELEPRANE: 919-541-8619
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Patent No. 5643774
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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: 7 Skyline Drive
Hawthorne
                                                                                                                                                   SOFTWARE: Patentin Relectorrent Application Dafa:
APPLICATION NUMBER: US/FILING DATE: 08-JUN-1994
                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 01-JUN-1999
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genom HYPOTHETICAL: NO
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                                                                                                 MEDIUM TYPE: Floppy dis
COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DO
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Matches 117; Conservative
                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                        CLASSIFICATION:
                                                  USA
                                                                    10532
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                                  STATE: N
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US-08-456-837-6
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                                                                                                                                                                                                                         Length 7218;
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Best Local Similarity 13.8%; Pred. No. 0.00012;
Matches 67; Conservative 200; Mismatches 220; Indels
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Patent No. 563949
SEMERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James N
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Hill, Dwight Steven
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
                TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
   (703)683-4109
                                                                                                                                                                     , CLONE: pT2gpt-F1s
US-08-232-463-14
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US-08-258-261B-6
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us-09-900-237-29.rni

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; ANTI-SENSE: NO US-08-457-342-6
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US-08-457-646A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 TGCCAGATCTGCGCCGACGGCCTGGGCACCACGTTGGACGGCGACGTCTTCACCGCCTGC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 CGCGCCATGGACGCCGACGCGCACGCCCTGAAGTCCGGGAGGCACGGGGCCGGGGACGTG 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 1.5%; Score 53.4; DB 1; Length 2 Best Local Similarity 52.5%; Pred. No. 0.00072; Matches 117; Conservative 0; Mismatches 106; Indels
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                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/456,837
FILING DATE: 01-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/457,205
FILING DATE: 01-JUN 1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-JUN 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 CAGGCCTGCCTCCAGTGCAAGACCAAGTACAAGCGCCACAGAG 276
             ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schupp, Thomas
Ligon, James M.
Beck, James Joseph
Hill, Dwight Steven
Ryals, John Andrew
Gaffney, Thomas Deane
Lam, Stephen Ting
Hammer, Phillip E.
                                                                                                                     ZIP: 10532
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 6, Application US/08457342
Patent No. 5662898
SERNEAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REPRENCE/DOCKET NUMBER: GGC J
TELECOMMUNICATION INFORMATION:
TELEPAN: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE:
US-08-456-837-6
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APPLICANT:
                                                                                                        COUNTRY:
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24526 GGGGCCTTGGGCGCCGGACGCCGCTCCAGAACCTTCTCGGACAACGCCGACGGCTACGGA 24585
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                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IED PC compatible
COMPOTER: IED PC compatible
COMPOTER: IED PC compatible
COMPOTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-JUN-1995
CLIASSIFICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: US 08/258,261
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GG 1506/CIP3
TELEFRAX: 919-541-8649
TELEFRAX: 919-541-8649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5%; Score 53.4; DB 1; 1
52.5%; Pred. No. 0.00072;
tive 0; Mismatches 106;
                    Genes for the synthesis of
antipathogenic substances
22
                                                                                                                                   ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
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APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for t
TITLE OF INVENTION: antipathoge
NUMBER OF SEQUENCES: 22
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APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 117; Conservative
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CACCGCCATCAACCACGACGCCCGTCGAGCGGT 24705
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1.0, Version #1.25
                                                                                                                                                                                  the synthesis of
                                                                                                                                                                                                     enic substances
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CLASSIFCATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 01-JUN-199
APPLICATION NUMBER: 08/
FILING DATE: 08-Jun-199
ATTORNEY/CAGNT INFORMATION
NAME: Elmer, James SCOT
REGISTRATION NUMBER: 36
                                                           Hill, Dwight S
Ryals, John An
Gaffney, Thoma
                                                                                                                                                                              TITLE OF INVENTION: Genes TITLE OF INVENTION: antip NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        ADDRESSEE: Ciba-Geigy C
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
COMPUTER: IBM PC compat.
OPERATING SYSTEM: PC-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Relacement Application Data:
APPLICATION UNMBER: US/
FILING DATE: 01-JUN-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMAT
TELEPHONE: 919-541-8619
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 28958 base pair
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 52.5%
Matches 117; Conservative
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                      Ligon, James M
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                                                                                                                                           Hammer, Philli
Uknes, Scott
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                         Lam, Stephen
Schupp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                           USA
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US-08-458-076A-6
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                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                  APPLICANT:
APPLICANT:
                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                        STATE:
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Pred. No. 0.00072;
0; Mismatches 106; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24706 ATCACCCCCCAACGCCACCTCCCAGCAGAAGGTCCTCCGGG 24748
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                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                              APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: GGC 1506/CIP3
TELECOMNUNICATION INFORMATION:
TELEPHONE: 919-541-8614
                                                                                                                                                                                                                                                                                                                                                                                          CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646A
FILING DATE: 01-UN-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-UN-1995
APPLICATION NUMBER: 08/457,205
FILING DATE: 08-UN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                    s: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08458076A; Patent No. 5698425; GENERAL INFORMATION:
                      Gaffney, Thomas Deane
    Ryals, John Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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52.5%;
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 52.5%
Matches 117; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
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                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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February 25, 2003, 18:32:29 ; Search time 181 Seconds
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11251.406 Million cell updates/sec
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/ CGRO_6/ptodata/2/pubpna/DSO7_NEW_PUB.seq:*
/ CGRO_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ CGRO_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ CGRO_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ CGRO_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/ CGRO_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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SUMMARIES

sequence 19, Appl Sequence 25, Appl Sequence 3, Appli Sequence 9, Appli Sequence 13, Appli Sequence 13, Appli Sequence 17, Appl Sequence 2530, Ap Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 21, Appli Sequence 9, Appli Sequence 9, Appli Sequence 29, Appl Description US-09-938-842A-559 US-09-938-842A-2530 US-09-900-237-17 US-09-900-237-23 US-09-900-237-27 US-09-900-237-27 US-09-900-237-27 US-09-900-237-2 US-09-900-237-2 US-09-900-237-2 US-09-900-237-2 US-09-900-237-2 US-09-900-237-2 US-09-900-237-29 US-09-900-237-25 US-09-900-237-25 US-09-900-237-7 US-09-900-237-9 US-09-900-237-13 US-09-900-237-13 US-09-900-237-13 П DB Length 3626 11733 3786 3786 33746 3317 3328 3328 2112 2112 11189 1029 1029 384 Query Match] 100.0 Score 3626 1364.6 1364.0 1340.2 1320.4 1320.4 1125.0 1125.0 1191.6 966.8 966.8 966.8 967.8 No. Result

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TCGAGCAACACCGGGGGGGGGGGGGGGGGGGGGGGGGGG	ISSULT 3 IS-09-900-237-25 Sequence 25, Application US/09 Sequence 25, Application US/09 Patent No. US20020120124a1 GENERAL INFORMATION: RAPLICANT: Allen, Stephen TITLE OF INVENTION: Plant Cel CURRENT APPLICATION NUMBER: 0 CURRENT APPLICATION NUMBER: 0 PRIOR FILING DATE: 1998-07-16 PRIOR FILING DATE: 1998-07-17 PRIOR FILING DATE: 1999-07-17 PRIOR FILING DATE: 1999-07-17 PRIOR FILING DATE: 2000-12-21 PRIOR FILING DATE: 2000-12-22 SOFTWARE: Microsoft Office 97 SEQ ID NO 25 LENGTH: 3563 TYPE: DNA OKGANIEN: Impatiens balsamie	tch 37.6%, bre 1364.4; DB 10; Length 3563; 31.08; Conservative Mismatches 1026; Indels 48; Gaps CTGAAGTCCGGAGGCACGGGG SGACGTGCCAGATCTGCGCGACGGCCTGGGC 140	CCCTGCGCGCTTCCCGGTTGCCGG CCCTGCGCGTTGCCGGTTGCCGG IIIII		GCTGACAGGATGCGCAGCTGGC
Oy 3342 TCGAGCA Db 1561 TCGAGCA OY 3402 GAGAAAC OY 3462 TTTTCAT OY 3462 TTTTCAT Db 1681 TTTTCAT	RESULT 3 US-09-900-237-25 Sequence 25, Application US/09 Patent No. US200201201241 GENERAL INFORMATION: APPLICANT: Allen, Stephen TITLE OF INVENTION: Plant Cel FILE REFERENCE: BB1170 US CIF CURRENT FILING DATE: 2001-07 PRIOR APPLICATION NUMBER: 60 PRIOR FILING DATE: 1999-07-14 PRIOR FILING DATE: 1999-07-14 PRIOR FILING DATE: 1999-07-15 PRIOR FILING DATE: 1999-07-15 PRIOR FILING DATE: 2000-12-21 NUMBER: 05 PRIOR FILING DATE: 2000-12-21 NUMBER: MICROSOFT OF 12 SEQ ID NO 25 LENGTH: 3563 TYPE: DNA CS-09-900-237-25	Query Match Best Local Similarity Matches 2108; Conser Qy 81 CTGAAGTCCGGGA	141 148 201 208	Oy 261 TACAAGG Db 268 TACAAAA Qy 321 GATGATG	Oy 381 GCTGACA Db 385 ACGCCAA OY 441 AAGTATC Db 445 AGGCATC OY 501 TACGTCC OY 505 GAAATTC
Db 421 CAAATGAGGTGAGAGATTTGGCCAGTCAGCACATTTGTTGCCTCCACTCTGATG 480 Qy 2262 GAATATGGTGGTGTTCCTCAGTCCTCCAGAATCTTTTGAAAGAAGCTATCCAT 2321	09 2442 GTCTATTGCATGCCCAAGCGCCAGGATCTGCCCCCATCAATCTTTCAGT 2501 Db 661 ATCTATTGCATGCCCAAGCGCCAGGTTTCAAGGGATCTGCCCCCATCAATCTTTCAGT 720 Qy 2502 CGTCTGAACCAAGCGCCCAGCTTTCAAGGGATCTGCCCCATCAATCTTTCAGCT 720 Qy 2502 CGTCTGAACCAAGTGCTGCGGTGGGCTCTTCTTTGATTTTCAGCCGGCAT 780 Qy 2562 TGCCCTTATGGTATGGCTACGGAGGCCCTCAAGTTCTTTTTTCAGCCGCAT 780 Qy 2562 TGCCCTTATGGTATGGCTACGGAGGCCCTCAAGTTCTTTTTTTT	Oy 2802 GTTGGCATTGACGAGTGGTGGAGGAATGAACAGTTCTGGGTCATTGGAGGTATCTCTGCA 2861	2922 ACTGTCACCTCAAAGGCTAATGACGAAGAGGCACTTTGCTGACCTCTACATGTCAAG 11111111111111111111111111111111111	QY 3042 GCTGGCACCTCTACGCCATCAACAGTGGTTACCAATCATGGGGGCCGCTCTTTGGGAAG 3101 L1	Oy 3162 AGGCAAAACCGCACACCGACGATTGTCATCGTCTGGGCTGTCCTCCTCGCTTCTATCTTC 3221

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1940 2000 2328 2448 2508 2568 2051 2037 2111 2097 2171 2291 2351 2411 2388 2471 2531 2591 2651 2628 GAAAAGCGTCCTGGGTTCCAGCACCACAAGAAGGCTGGTGCCATGAATGCCCTTGTTCGT 1700 CCAGAGATTAGCAACTTGGCCAGTATCTGGTTCATTGCGCTCTTCCTTTCAATTTTGGCC 2771 AACAACAGCAAGGCTGTCCGAGAAGCTATGTGCTTCCTAATGGATCCAAACCTAGGTCCG CCGCTTCTAGTCTATTGTATATTGCCTGCTATCTGTCTGCTCACTGGAAAGTTCATCATG **AAGAAGGCAAGCAAGTCAAAGAAAAGGAGCTCAGATAAGAAAAAGTCGAACAAGCATGTG** GGTTCTGTTGAAATTCTTTTCAGCCGGCATTGCCCCTTATGGTATGGCTACGGAGGGCGC GTCTCAGCTGTCCTTACTAATGGACAATACATGTTGAATCTTGATTGTGATCACTACATC GCAAACAGGAACACTGTCTTTTTGATATTAACTTGAGGGGCCTTGACGCATTCAAGGA CCAATTAAGGCGAAGAA-----GCCAGGTTTCTTGGCATCACTATGTGGGGGCCAAG GICTTAACAGAGGAGGATTGGAACCGAATATCATCATCAAGAGCTGTTGCGGCTCGAGG GACAGTICTGITCCAGTATICAATCTCGAAGACATAGAGGAGGGTGTTGAAGGTGCTGGG GAATGGGGAACTGATTGGTTGGATCTATGGATCTGTCACAGAAGATATTCTTACTGGA CCAGAATCTCTTTTGAAAGAAGCTATCCATGTCATAAGTTGTGGCTATGAGGACAAGTCT TCTGCAACCCTCTTGAAAGAAGCAATCCATGTTATTAGCTGTGGGTACGAGGACAAGACT TICAAGAIGCACGCAAGAGGCIGGCGTICAGICTAIIGCAIGCCCAAGCGCCCAGCITIC AAGGGATCTGCCCCCATCAATCTTCAGATCGTCTGAACCAAGTGCTGCGGTGGGCTCTC CAAGTCTGTTATGTGCAGTTCCCACAAAGGTTTGATGGGATTGATAGGAATGATCGATAT TCAGCAGCATTTGTTGCCTCCACTCTGATGGAATATGGTGGTGTTCCTCAGTCCTCCACT 1618 1798 2001 2098 2209 2269 2352 2412 2389 2652 2629 2712 1678 1738 1858 1941 1918 1978 2052 2038 2112 2172 2232 2292 2329 2472 2449 2532 2509 2592 2569 1641 1701 1761 1881 Q7 Db 92 03 03 Db Db 97 97 97 QV Db g Óλ g g q g Qγ g οy Dp QY 9 9 9 9 g Οý QΥ QΥ Óλ Ω

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δý	1644	AAGCGTCCTGGGTTCCAGCACACACAAGAAGGCTGGCATGAATGCCGTTGTTCGTGTC 1703	
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QQ	2054	AACAGGAACGITGITGITTTTGACATCAACATGAAAGGITTGGACGGTATTCAAGGACC 2113	
Q Dp	1944	GITTATGIGGGAACTGGITGTGITTTCAACAGAACAGCTATCTATGGTTATGAGCCCCCA 2003 	
Qy	2004	ATTAAGGCGAAGAAGCCA	
δy	2037	209	
οp	2234	29	
οy	2096	GTCGAACAAGCATGTGGACAGTTCTGTTCCAGTATTCAATCTCGAAGACATAGAG 2150	
q	2294	AGATTATTTTCAAGAAAGCAGAAAACCCATCTCCTGCATATGCTTTGGGTGAAATTGAT 2353	
Oy Dp	2151	GAGGGTGTTCAAGGTGCTGGGTTTGATGATGAGAAATCAGTTCTCCATGTCTCAAATGAGC 2210 	
yo d	2211	27	
λō	' (1	GGGGTGTTCTCCAGTCCTCCAGAACCTTTTGTAAAAGCTATCCATGTCATAAGT 2330	
QQ	2468	GGGACCCTGAAGAGGGGAAGTCCAGGTTCTCTTCTGAAGGAAG	

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RESULT 5 US-09-900-237-3 ; Sequence 3, Application US/09900237 œ

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                                                                                                                                                                                                                      Score 1320.4; DB 10,
Pred. No. 0;
0; Mismatches 1071;
       GENERAL INFORMATION:
APPLICANT: Allen, Stephen
TITLE OF INVENTION: Plant Cellulose Synthases
FILE REFERENCE: BB1170 US CIP
CURRENT APPLICATION NUMBER: US/09/900,237
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/092,844
PRIOR APPLICATION NUMBER: PCT/US99/15871
PRIOR APPLICATION NUMBER: PCT/US99/15871
PRIOR APPLICATION NUMBER: PCT/US99/15871
PRIOR APPLICATION NUMBER: 09/720383
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEO ID NOS: 33
SEO ID NO 3
LENGTH: 3776
                                                                                                                                                                                                                        36.4%;
64.5%;
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Best Local Similarity 64.55
Matches 2135; Conservative
  Patent No. US20020120124A1
                                                                                                                                                                                         ; ORGANISM: Zea mays
US-09-900-237-3
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35.1%;
63.9%;
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SOFTWARE: Microsoft Office 97
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Matches 2110; Conser
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CORGANISM: Zea mays
US-09-900-237-9
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                              TATTAACTTGAGGGGCCTTGACGGCATTCAAGGACCAGTTTATGTGGGAACTGGTTGTGT
                                         -----AAGCCAGGTTTCTTGGCATCACTATGTGGGGGCAAGAAAA
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Petent No. US20020120124A1
GENERAL INFORMATION:
APPLICANT: Allen, Stephen
TITLE OF INVENTION: Plant Cellulose Synthases
FILE REPERENCE: BB1170 US CIP
CURRENT APPLICATION NUMBER: US/09/900,237
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/092,844
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-13
PRIOR FILING DATE: 1998-07-13
PRIOR FILING DATE: 2000-12-21

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371 GGGCAC	287 GATCCG	347 TGCATC' 491 CGGCCA'	407 GAACAC 539 GAGCTA	467 CTCCAA 573 CCACAA	527 GATGTC 623 AATGGT	587 CATCAG 683 GGGAAA	647 CTCCGG	707 GGACAA 803 GATGGA	767 AGCTAC' 863 TGATGA'	827 AACTCG 	887 AATGGT 962 GATGAT	947 TCCTGT 1022 TCCGGT	1007 TTTATC 	1067 TGATAG 1142 AGACCG	1127 CATATT	1187 GCTATC 1262 TCTATC	1247 CGGAGC 322 TGGTGC	
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GGCAGCAAACTTTGTTAGGGAGAGGAGAGAAT GCTCCGAGTCTCTGCTGTACTAACAAATGCTCC CITITICCIGITGCTGCTTTGCCATAGGAAGCA CAACAAAATTAGAAAAGAAATTIGGCCAATC CCAGCCTTCATTTGTTAAAGACCGCCGGGCCAT GTCTCGTGAAAGCGTCCTGGGTTCCAGCACCA TTCTAGAGAGAACGACCAGGCTATAACCATCA AGGTCCGCAAGTCTGTTATGTGCAGTTCCCACA FGAGCCCCCAATTAAGGCGAAGAAGCCA---rgatgccccaaaacaaagaagccaccatcaag CTTGGCATCACTATGTGGGGGCAAGAAGAAGCC FARGAAAAAG-----TCGAACAAGCATGTGGA AGATGGCACACCATGGCCAGGAAACAATACCAG CCTTGGTCACAGTGGTGGCCTTGATACTGAGGG **IGTICGIGICICAGCIGICCTIACIAAIGGACA** CTACATCAACAACAGCAAGGCTGTCCGAGAAGC **ICGATATGCAAACAGGAACACTGTCTTTTTGA** PCAAGGACCAGTTTATGTGGGAACTGGTTGTGT GAAGAAAAGTTATTTTTTCAAGAAAGAAGA GACATAGAGGAGGGTGTTGAAGGTGCTGGGTT CAAATGAGCTTAGAGAGAGATTTGGCCAGTC SGAATATGGTGGTGTTCCTCAGTCCTCCACTCC GTCATAAGTTGTGGCTATGAGGACAAGTCTGA TTTCAACAGAACAGCTATCTAT GACTTGCAACTGCTGGCCCAAG **AAGCAAGTÇAAAGAAAAGGAGC** AAAGAAGACTACCAAACCCAAA CAGTICIGITCCAGTATICAAT TGATGAGAAATCAGTTCTC TGCTTCTCTTTGAAAGAAGCT CTGGGGAAAAGAGATTGGCTGG TATTAACTTGAGGGGCCTTGAC ||| ||| ||| || || || TATCAACATGAAAGGTTTGGAT GAACCAATCCCCTGCATATGCT TGAGAATGAAAAGGCCGGTATT AGCAGCATTTGTTGCCTCCACT AGAATCTCTTTTGAAAGAAGCT ATGGGGAACTGAGATTGGTTGG TTCTGTTTTTGTTACATCCACA GGATCATCCTGGAATGATTCAG GAAAATTGATTACCTGAAAGA GAAGAGAATATGAAGAATT GAAGAGAGTATGAGGAATT AGTCCCCGAGGAAGGATGGATC TGATCATCCTGGAATGATTCAC TAATGAGCTCCCCCGTTTAGT AAATGAACTGCCACGATTGGT CAAGAAGGCTGGTGCCATGAA ATACATGTTGAATCTTGATTG TATGTGCTTCCTAATGGATCC AATGTGTTTTATGATGGACCC **AAGGTTTGATGGGATTGATAG**(1682 1787 1862 2102 2222 2276 1502 1562 1607 1922 1982 1961 2060 2162 2114 2234 2336 2294 2354 1367 1487 1547 1622 1667 1727 1802 1847 1907 2022 2174 2456 1427 δy qq δy Dp qq 92 DB δŽ g QΥ QQ δ g QY g δλ g δ Dp δλ g δ gg οy g δ q ŏ g οy qq δ οy g δ q

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Pred. No. 0;
0; Mismatches 685;
CURRENT APPLICATION NUMBER: US/09/900,237
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION UNMBER: 60/092,844
PRIOR FILING DATE: 1998-07-14
PRIOR PELING DATE: 1999-07-13
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFUR PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 13
LENGTH: 3517
    us/09/900,237
                                                                                                                                                                                                                    Query Match 34.7%;
Best Local Similarity 70.4%;
Matches 1768; Conservative
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ORGANISM: Glycine max
US-09-900-237-13
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Sequence 13, Application US/09900237
Sequence 13, Application US/09900237
General INFORMATION:
APPLICANT: Allen, Stephen
ATILE OF INVENTION: Plant Cellulose Synthases
FILE REFERENCE: BB1170 US CIP
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CTCAAAGGCTAATGACGAAGAGGCGACTTTGC 2962 TECCTTCTGGGTGATTGTTCACTTATACCCATT 3142 ACGCACACCGACGATTCTCATCGTCTGGGCTGT 3202 TIGCCGTCTTTCAGGGTCTTCTGAAGGTGCTTGC 2902 GCTTCTCATCCTCCGACGACCATTTTGATCAT 3022 ACTITITATION NO SACTOR CTCCTACGCCATCAACAGTGGTTACCAATCATG 3082 ACTCACTGACAAATTCATGCCACGGATTAG 2701 CAGCCTCTATCTAGAAAGTCCCCATTGCTTCC 866 ore 1215.6; DB 10; Length 3328; ed. No. 0; Mismatches 739; Indels 21; (e Synthase and Promoter onucleotide 838,539 ion 4.0 81 48

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2486 2546 2341 2843 2126 2186 1981 2246 2306 2101 2366 2161 2426 2221 2281 2603 2401 2663 2461 2723 2521 2783 2581 2641 2903 2701 2963 GAGCTCTACATGTTCAAGTGGACGACGGTTCTCATCCCTCCGACGACCATTTTGATCATT 3023 AGGAACACAGTTTTCTTTGATGTTAACATGAAAGGTCTTGATGGAATCCAAGGGCCAGTT 1756 2282 ATCAATCTGTCTGATCGGTTGCACCAGGTTCTTCGATGGGCTCTTGGATCTGTTGAAATT TCAAAGAAAAGGAGCTCAGATAAGAAAAAGTCGAACAAGCATGTGGACAGTTCTGTTCCA GAACCTAAAGATCCATCAGAGCTTTATAGGGATGCAAAACGGGAAGAACTTGATGCTGCC GTATTCAATCTCGAAGACATAGAGGAGGGTGTTGAAGGTGCTGGGTTTGATGATGAAAA GCCTCCACTCTGATGGAATATGGTGGTGTTCCTCAGTCCTCCACTCCAGAATCTCTTTTG 2042 GAATCTACACTAATGGAGAAATGGAGGAGGAGGATGAATCTGCCAACCCTTCCACACACTAATC AAAGAAGCTATCCATGTCATAAGTTGTGGCTATGAGGACAAGTCTGAATGGGGAACTGAG ATTGGTTGGATCTATGGATCTGTCACAGAAGATATTCTTACTGGATTCAAGATGCACGCA ATCAATCTTTCAGATCGTCTGAACCAAGTGCTGCGGTGGGCTCTCGGTTCTGTTGAAATT CITITCAGCCGGCATTGCCCCCTTATGGTATGGCTACGGA----GGGCGCCTCAAGTTCCTG GAGAGATTCGCTTACATCAACACCACCATTTACCCACTAACCTCTCTCCCGCTTCTAGTC TATTGTATATTGCCTGCTATCTGTCTGCTCACTGGAAAGTTCATCATGCCAGAGATTAGC AACTTGGCCAGTATCTGGTTCATTGCGCTCTTTCCATTTTCGCCACTGGTATCCTT GAGATGAGGTGGAGTGTTGGCATTGACGAGTGGTGGAGGAATGAACAGTTCTGGGTC ATTGGAGGTATCTCTGCACATCTGTTTGCCGTCTTTCAGGGTCTTCTGAAGGTGCTTGCC GGTATCGACACCAACTTCACTGTCACCTCAAAGGCTAATGACGAAGAAGGCGACTTTGCT AGAGGCTGGCGTTCAGTCTATTGCATGCCCAAGCGCCCAGCTTTCAAGGGATCTGCCCCC 2642 2462 2582 2759 2367 2664 2522 2844 2102 2162 2427 2402 2724 2784 1697 1947 1757 2007 1817 2067 1877 2127 1937 2247 2307 2222 2487 2547 2604 2904 qq g qq 8 QΥ Q Qy Db 0.7 0.0 0.7 0.7 임 QΣ q οy Q ōλ g οy g οy δ Ω g οy ΩD ÓΥ q QY δ Ω δy g δy q us-09-900-237-29.rnpb

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	2938 3203 2998	3263 3058	*	(C) (G) (G)	∂ ã		GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING DS OF USE 3,842A D1		(C) II	(0)	DB 9; Length 3255; Q3 754; Indels 12; Gaps 2; Dt	TGCTTCCTCCAAAATAA 876	936	966		1116

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RESULT 10

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        Sequence 2530, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION

APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Ann, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLA
TITLE OF INVENTION: STAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-03-17

FROM REPROBLEMENT NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER: OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                        Score 1191.4;
Pred. No. 0;
0; Mismatches
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68.8%;
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Matches 1687; Conservative
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US-09-938-842A-2530
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CTTATGGTATGGCTACGGGGGGCCTCAAGT 2599	Synthases 00,237 4 15871
Oy 2540 TGAAATTCTTTCAGCCGGCAT	RESULT 11 US-09-900-237-17 Sequence 17, Application US/099 Fatent No. US2002012012441 GENERAL INFORMATION: APPLICANT: Allen, Stephen TITLE OF INFORMATION: FILE REFERENCE: BB1170 US CIP CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 2001-07- PRIOR APPLICATION NUMBER: OF PRIOR APPLICATION NUMBER: OF PRIOR APPLICATION NUMBER: OF PRIOR RILING DATE: 1999-07-13 PRIOR FILING DATE: 1999-07-13 PRIOR PELING DATE: 1999-07-13 PRIOR PELING DATE: 1999-07-13 PRIOR PELING DATE: 1999-07-13 SPRIOR FILING DATE: 1999-07-13 PRIOR PELING DATE: 1999-07-13 SEC ID NO 17 LENGTH: 2890 LENGTH: 2890 TYPE: DNA ORGANISM: Glycine max US-09-900-237-17
1475 TAAGGCATTGAAAGTCCCCGAGGAGGATGGATCATGCAAGATGGCACCACTGGCCCGG 1534	2180 TGAGAAATCAGTTCTCAAATGAGCTTAGAGAAGATTTGGCCAGTCGGCG 2239 2136 AGAACAGTCAACCGAGGAATGAATGAGTTGGAGAAGAATTTGGCCAGTCCTGT 2195 2240 ATTGTTGCCTCCACTCTGATGGAATATGGTGGTTCCTCAGTCCTCCTGT 2195 2240 ATTGTTGCCTCCACTCTGATGGAATATGGTGGTTCCTCAGTCCTCCAGAATC 2299 111 1 1 1 1 1 1 1 1

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1 32.6%; Score 1183.4; DB 10; Length 2890; Similarity 70.4%; Pred. No. 0; 31; Conservative 0; Mismatches 671; Indels 15; Gaps 3;	ATCCTGTGCGTAATGCATACCCACTGTGGCTTTTATCTGTTATGTGTGGAGATTTGGTTTG 1005	CTTTATCCTGGATACTGGATCCGAAGTGGTTTCCAATCAACCGGGAGACCTACC 1065 	TTGATAGACTGGCTTTAAGGTATGACCGAGAAGGTGAACCGTCTCAGTTGGCTGCTGTTG 1125 	ACATATTIGICAGIACAGICGACCCCTIGAAGGAGCCACCTAICGICACCTGCCAACACTG 1185	TGCTATCCATTCTTGCTGTTGATTATCCCGTGGACAAGGTCTTGCTATGTATCTGATG 1245	ACGGAGCTTCAATGCTGACTTTTGACGCATTGGCTGAGACTTCAGAGTTTGCTAGGAAAT 1305 	GGGTACCATTIGIGAAGAAGTAIGACATIGAACCCAGAGCICCCGAGTITITACITITGCC 1365 	AGAAAATTGATTACCTGAAAGACCAACCCTTCATTTGTTAAAGACCGGGGCCA 1425 	TGAAGAGAATATGAAGAATTTAAAATCAGGATAAATGCCCTAGTTTCTAAGGCATTGA 1485 	AAGTCCCCGAGGAAGGAIGGATCATGCAAGATGGCACATGGCCAGGAAACAATACCA 1545 	GGGATCATCCTGGAATGATTCAGGTTTTCCTTGGTCAGTGGTGGCCTTGATACTGAGG 1605	GTAATGAGCTCCCCCGTTTAGTTTATGTGTCTCGTGAAAAGCGTCCTGGGTTCCAGCACC 1665 	ACAAGAAGGCTGGTGCCATGAATGCCCTTGTTCGTGTCTCAGCTGTCCTTACTAATGGAC 1725	AATACATGTTGAATCTTGATTGATCACTACAACAACGCAGGCTGTCCGAGAG 1785 	CTATGTGCTTCCTAATGGATCCAAAGCCTAGGTCGGAAGTCTGTTATGTGCAGTTCCCAC 1845 	AAAGGTTTGATGGGATTGATAGGAATGGTAGGGAACACTGGTCTTTTTTG 1905	ATATTAACTTGAGGGCCTTGACGGCATTCAAGGACCAGTTTATGTGGGAACTGGTTGTG 1965 	TTTCAACAGAACAGCTATCTATGGTTATGAGCCCCCAATTAAGGCGAAGAAGC 2019
Query Match Best Local Simi Matches 1631;	946 ATCCTGT 12 ACCCAGT	1006 CTTTATC 72 CTGTATC	1066 TTGATAG 132 TTGATCG	1126 ACATATT 192 ACGTCTT	1186 TGCTATC 252 TTCTATC	1246 ACGGAGC 312 ATGGTGC	1306 GGGTACC 372 GGGTTCC	1366 AGAAAAT 432 AGAAGAT	1426 TGAAGAG 492 TGAAGAG	1486 AAGTCCC 552 AGGTTCC	1546 GGGATCA 612 GGGATCA	1606 GTAATGA 672 GAAATGA	1666 ACAAGAA 732 ACAAAAA	1726 AATACAT 792 CCTATCT	1786 CTATGTG 852 CTATGTG	1846 AAAGGTT 	1906 ATATTAA 972 ATATTAA	1966 TITICAA
N N N	Qy	QY DP	ζ, dg	Qy Dp	Qy . dd	Qy Db	Qy	Qy Dp	Qy Dp	Qy Dp	Qy Dp	Qy Db	Q Dp	oy O	Qy Db	Qy Db	Qy Db	δλ

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	FILE REFERENCE: BB1170 US CIP. CURRENT APPLICATION NUMBER: US/09/900,237 CURRENT FILING DATE: 2001-07-06	oy da	1874 TCGATATY 791 TCGATATY
	IIOR APPLICATION NUMBER: 60/092,844 INCR FILING DATE: 1998-007-14	δy	1934 TCAAGGA
	AION APPLICATION NUMBER: PCI/US99/128/1 AION FILING DATE: 1999-07-13	QQ	851 ACAAGGG
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CAAGAAATCGAAACCAAAGAAGGAGAAGAAGAA 1030 GGTTGGTTGGATCTATGGATCTGTCACAGAGA 2398 AGAAGCTATGTGCTTCCTAATGGATCCAAACCT 1813 TGTGTTTTCAACAGAACAGCTATCTATGGTTA 1993 TGAGGGTAATGAGCTCCCCCGTTTAGTTTATGT 1633 TGGACAATACATGTTGAATCTTGATTGTGATCA 1753 FTTTGATATTAACTTGAGGGGCCTTGACGGCAT 1933 GGGAAAAGCTTGTAACTGTTGGCCTAAATGGTT 970 TGTGCGAGACCATCCTGGCATGATTCAGGTTTT 490 GCACCACAAGAAGGCTGGTGCCATGAATGCCCT CCCACAAAGGTTTGATGGGATTGATAGGAATGA AGG------TITCTIGGCATCACTAIG ATCAGTTCTCATGTCTCAAATGAGCTTAGAGAA **IGCCTCCACTCTGATGGAATATGGTGGTGTTCC** GCTTCTACTCTTCTAGAAGATGGTGGAGTCCC GAAAGAAGCTATCCATGTCATAAGTTGTGGCTA SAAGAGGCTGGCGTTCAGTCTATTGCATGCCCAA CATCAATCTTTCAGATCGTCTGAACCAAGTGCT TCTTTTCAGCCGGCATTGCCCCTTATGGTATGG GAGATTCGCTTACATCAACACCCACCATTTACCC AAAGAAAAGGAGCTCAGATAAGAAAAAGTCGAA AGTATTCAATCTCGAAGACATAGAGGAGGGTGT SACTCCTTGGCCTGG CAAGAAGAAGGCAAGG **FGAAAAGCGTCCTGG** rGTCTCAGCTGTCCT! CAACAACAGCAAGGC CAACAATAGCAAAGC SCAAGTCTGTTATGT FGCAAACAGGAACAC | | ||| |||| |TCCAACCGGAATGT ACCAGTTTATGTGGG CCCAATTAAGGCGAA ACCAGTCACTAAGAA CTGTTGTGGGTCCAG GCATGTGGACAGTTC AAATAGGGAAGCATC **rgCTGGGTTTGATGA** A----TTGAACTC TGGCCAGTCAGCAGC CTCCACTCCAGAATC | ||||| | | TGCAACTCCTGCAGC CAAGTCTGAATGGGG TACTGGATTCAAGAT GACTGGATTCAAGAT AGCTTTCAAGGGATC CGCATTTAAGGGGTC GGCTCTCGGTTCTGT ||| |||||||| TGGACAGTCTCCAGT TAAAACAGAATGGGG AGGGCGCCTCAAGTT PCACAGTGGTGGCCT GAAATTATGCTATGT

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Pred. No. 5.2e-272;
0; Mismatches 507;
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71.6%;
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Matches 1316; Conservative
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CTAAGGCATTGAAAGTCCCCGAGGAAGGATGGATCATGCAAGATGGCACACCATGGCCAG
        CTGTCTTTTTTGATATTAACTTGAGGGGCCCTTGACGCATTCAAGGACCAGTTTATGTGG
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; TYPE: DNA ; ORGANISM: Glycine max US-09-900-237-27	Query Match 22.7%; ore 821.4; DB 10; Length 1560; Best Local Similarity 78.6%; ad. No. 1.4e-229; Matches 1010; Conservative Mismatches 266; Indels 9; Gaps	Qy 1093 GAGAAGGTGAACCGTCTCAGT3 \$CTGTTGACATATTGTCAGTACAGTCGACCCCT 1152	Oy 1153 TGAAGGAGCCACCTATCGTCAC AACACTGTGCTATCCATTCTTGCTGTTGATTATC 1212	Qy 1213 CCGTGGACAAGGTCTCTTGCTA CTGATGACGGAGCTTCAATGCTGACTTTTGACG 1272	QY 1273 CATTGGCTGAGACTTCAGAGTT AGGAAATGGGTACCATTGTGAAGAAGTATGACA 1332	OY 1333 TTGAACCAGAGCTCCGAGTT TTTGCCAGAAATTGATTACCTGAAAGAAG 1392	QY 1393 TCCAGCCTTCATTGTTAAAGA & GGGCCATGAAGAGAATATGAAGAATTTAAAA 1452 	QY 1453 TCAGGATAAATGCCCTAGTTTG CATTGAAAGTCCCGGAGGAAGGATGGATGGTCATGC 1512	QY 1513 AAGATGGCACACCATGGCCAGG AATACCAGGGATCATCCTGGAATGATTCAGGTTT 1572	QY 1573 TCCTTGGTCACAGTGGCCT ACTGAGGGTAATGAGCTCCCCGGTTTAGTTTATG 1632	Qy 1633 TGTCTCGTGAAAAGCGTCCTGG RACACCACAAGAAGGCTGGTGCCATGAATGCCC 1692	OY 1693 TIGHTCGFGTCTCAGCTGTCCT MATGGACAATACATGTTGAATCTTGATTGTGATC 1752	QY 1753 ACTACATCAACAAGGG CGAGAAGCTATGTGCTTCCTAATGGATCCAAACC 1812	OY 1813 TAGGECGGAAGTCTGTTATGE OTCCCACAAAGGTTTGATGGGATTGATAGGAATG 1872	OY 1873 ATCGATATGCAAACAGGAACAC TTTTTGATATTAACTTGAGGGCCTTGACGGCA 1932	OY 1933 TTCAAGGACCAGTTTATGTGGG GTTGTGTTTCAACAGAACAG	OY 1993 ATGAGCCCCCAATTAAGGCGAAAAGCCAGGTTTCTTGGCATCACTATGTGGGG 2046	QY 2047 GCAAGAAGAAGGCAAGCAA AGAAAAGGAGCTCAGATAAGAAAAAGTCGAACA 2103
QY 2545 TICTITICAGCCGCATTGCCCTTATGGTATGGCTACGGAGGCGCCTCAAGTTCCTGG 2604	OY 2605 AGAGATICGCITACAICACACCACATTACCCACTAACCICICCCGCITCIAGICI 2664	OY 2665 ATTGTATATTGCCTGCTATCTGTCTCACTGGAAAGTTCATCATCAGCCAGAGATTAGCA 2724	OY 2725 ACTIGGCCAGTATCIGGITCATIGGCTCTTCCATTCAATTTTCGCCACTGGTATCCTTG 2784	OY 2785 AGAIGAGGIGGAGTGGTGTTGGCATTGACGAGTGGTGGAGGAATGAACAGTTCTGGGTCA 2844	QY 2845 TTGGAGGTATCTCTGCATCTGTTTGCCGTCTTTCAGGGTCTTCTGAAGGTGCTTGCCG 2904 1	QY 2905 GTATCGACACCAACTTCACTGTCACCTCAAAGGCTAATGACGAAGAAGGCGACTTTGCTG 2964	OY 2965 AGCTCTACATGTTCAAGTGGACGACGCTTCTCATCCCTCCGACCACTTTGATCATTA 3024	OY 3025 ACATGGTTGGTGGTGGCACCTCCTACGCCATCAACAGTGGTTACCAATCATGGG 3084 1	OY 3085 GGCGGCTCTTTGGGAAGCTCTTGCTTGTGGGTGATTGTTCACTTATACCCATTCC 3144	OY 3145 TCAAGGGTCTTATGGGCAGGCAAAACCGCACCCACGATTGTCATCGTCTGGGCTGTCC 3204 1	OY 3205 TCCTCGCTTCTATCTTCTCCTGCTGCGCTCTGTTGATCCATTCACTACCCGTCTCG 3264 1	Qy 3265 CTGGCCCAAATATCCAAACCTGTGGCATCAACTGCTAG 3302 Db 1796 ACAAATTAACCAATGGTCAATGTGGCATCAACTGTTAG 1833	RESULT 14 US-09-900-237-27	; Patent No. US20020120124Al ; GENERAL INFORMATION: ; APPLICANT: Allen, Stephen : TTFLE OF INVENTION: Diant Callulose Sunthasse	; FILE REFERENCE: BB110 US CIP ; CURRENT APPLICATION NUMBER: US/09/900,237 ; CURRENT FILING DATE: 2001-07-06	; PRIOR FILING DATE: 1998-07-14 ; PRIOR APPLICATION NUMBER: PCT/US99/15871 ; PRIOR FILING DATE: 1999-07-13 · PRIOR FILING DATE: 1999-07-13	FRIOR FILING DATE: 2000-12-21 NUMBER OF SEQ ID NOS: 33 SEGOTOR OF SEQ ID NOS: 37	; SEQ ID NO 27 ; LENGTH: 1560

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Pred. No. 7.4e-143;
0; Mismatches 212;
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Patent No. US20020120124A1

GENERAL INFORMATION:
APPLICANT: Allen, Stephen
TITLE OF INVENTION: Plant Cellulose Synthases
FILE REPERENCE: BB1170 US CIP
CURRENT APPLICATION NUMBER: US/09/00,237

CURRENT FILING DATE: 1098-07-14

PRIOR FILING DATE: 1998-07-14

PRIOR FILING DATE: 1999-07-13

PRIOR APPLICATION NUMBER: 09/720383

PRIOR FILING DATE: 1999-07-13

PRIOR SEQUEN NUMBER: 09/720383

NUMBER OF SEQ ID NOS: 33

SOFTWARE: MICROSOFT Office 97

FENCINE APPLICATION NUMBER: 09/720383
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Best Local Similarity 75.5
Matches 652; Conservative
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SID52/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SID52/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SID52/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

SUMMARIES

	Description	Corn cellulose syn	Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	DNA encoding a mai	Arabidopsis thalia	Arabidopsis thalia	Herbicidally activ	Arabidopsis cellul	Arabidopsis thalia
	ID	AAU10496	AAY84108	AAY84114	AAY84119	AAY84121	AAG48734	AAG48733	ABB93356	AAW33819	AAG48735
	DB	23	21	21	21	21	21	21	33	19	21
	Query Match Length DB ID	1079	1077	1077	1043	1076	1054	1065	1065	1065	959
dР	Query	93.9	93.7	93.7	91.0	89.0	78.4	78.4	78.4	77.9	72.9
	Score	5423.5	5415.5	5415.5	5255.5	5143	4530	4530	4530	4499	4209.5
	Result No.	1	7	m	4	2	9	7	80	σ	10

	11 12 13	3993.5 3993.5 3993.5		07	21 21 21	AAY84110 AAY84112 AAY84117		Amino acid sequenc Amino acid sequenc Amino acid sequenc
	14 15 16	3981 3981 3981 3981	688.9 6.89.9 6.90.9	1075 1075 1075	277	AAY84109 AAY84115 AAY84120 AAW33817		Amino acid sequenc Amino acid sequenc Amino acid sequenc Arabidosis cellul
	118	3963.5 3953.5 3853.5		8888	133	ABB93199 AAW33820 AAV84113		Herbicidally active Arabidopsis cellul
	21	3844.5 3844.5		160	21	AAY84118 AAY58834		Amino acid sequenc Corn cellulose syn
	23	3820.5 3820		03	21	AAY58837 AAY84107		Soybean cellulose Amino acid sequenc
	26	3818		80	21	AAY84111 AAY84116		Amino acid sequenc Amino acid sequenc
	27	3818 3818		08 14	21	AAY58835 AAY58832		Corn cellulose syn
	30	3801 3778.5		02	23	ABB93522 ABB91880		Herbicidally active Herbicidally active
	31	3777.5 3746		03	19 23	AAW73309 ABB93701		Cellulose synthase Herbicidally activ
	33	3666.5		80	23	ABB93304		Herbicidally activ
	3.5	3636		800	733	ABB93949		Herbicidally activ
	37	3579		80	23	ABB91831		Arabidopsis cellul Herbicidally activ
	38	3566.5		808	22	AAB37895		Arabidopsis thalia
	40	3482		974	13	AAW73308		Cellulose synthase
	41	3477 3408.5		974 955	13	AAB16338		Cotton cellulose s Eucalyptus grandis
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	45	3157		946	22	AAB37893		opulus tre
						ALIGNMENTS		
RESULT 1	1LT 0496	-1.0						
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Y Y	AA	AAU10496;						
4 E S	14	-FEB-2002	(firs	st entry	γ)			
OE Y	Corn	cellul	ose s	ynthase	Cqrae19	e19/cesA-9.		
KW KW	Corn; stal) hand]	cellu quali	ulose syr ity; impr bility; '	nthase roved transg	; Cdp stand enic	pgs45; cesA-3; (d; silage; perice plant; immunoge	Cqrae19; cesA: :icarp; kernel b gen.	,8-9; hardening;
90	Zea	a mays.						
V NA	W02	200179516	-A2.					
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PF	13	-APR-2001	.,	001WO-US11	951.			
PR S	14	-APR-2000	; 2000US	JS-0550	483.			
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PI	Dh	Dhugga KS,	Helentj	aris	TG;			
R R R	X X	WPI; 2002-0 N-PSDB; AAS	41338 16458	/05.				
PT PT	Nei	New cellulose synthase improving stalk quality	se synt talk gu	chase p ality	olyp or s	polypeptides and po y or silage, and in	polynucleotides n increasing co	les, useful in concentration of

N

The invention relates to isolated nucleic acids encoding two cellulose synthase proteins from corn, Cdpgs45 (cesA-3) and Cqrael9 (cesA-9).

Also disclosed are a recombinant expression cassette comprising the polynucleotide (operably linked to a promoter) a host cell comprising the recombinant expression cassette and a transgenic plant comprising the recombinant expression cassette and a transgenic plant comprising the recombinant expression cassette. The nucleic acid is useful in the improvement of stalk quality for improved stand or silage, and in the increased concentration of cellulose in the pericarp, hardening the kernel, and thus improving its handling ability. The nucleic acids may also be used as probes or amplification primers in the detection, quantification or isolation of gene transcripts, as probes in detecting deficiencies in the level of mRNA, for detecting gene mutations or alliants, for monitoring up regulation of expression or changes in enzyme activity in screening assays, for site directed mutagenesis, and in sense or antisense suppression of one or more genes in a host cell, tissue or plant. The polypeptides may be used in assays for or brayme agonists or antagonists, and as immunogen or antigen to obtain antibodies specifically immunoreactive with the protein. cellulose in the pericarp, hardening the kernel for improved handling Claim 3; Page 85-87; 88pp; English invention ability

1079 AA; Sequence

ï 180 181 APFPYVNHSPNPSREFSGSIGNVAWKERVDGWKMKQDKGAIPMTNGTSIAPSEGRAATDI 240 300 360 420 420 480 480 61 CLOCKTKYKRHRGSPAIRGEEGDDTDADDGSDFNYPASGTEDQKQKIADRMRSWRMNTGG 120 IDRNDRYANRNTVFFDINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKKPGFLASL 660 1; Gaps 1 MDGDADALKSGRHGAGDVCQICADGLGTTLDGDVFTACDVCRFPVCRPCYEHERKEGTQA 60 9 121 SGDVGRPKYDSGEIGLTKYDSGEIPRGYIPSVTNSQISGEIPGASPDHHMMSPTGNIGRR SGNVGHPKYDSGEIGLSKYDSGEIPRGYVPSVTNSQMSGEIPGASPDHHMMSPTGNISRR AYPLWLLSVICEIWFALSWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVS TVDPLKEPPIVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFDALAETSEFARKWVPFV KKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVSKALKVPEE **GWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAG** AMNALVRVSAVLTNGQYMLNLDCDHY INNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDG DB 23; Length 1079; 37; Indels 93.9%; Score 5423.5; 92.2%; Pred. No. 0; 46; Mismatches Query Match
Best Local Similarity 92.2
Matches 996; Conservative 121 181 301 361 361 421 421 481 541 601 481 ð g à g à 셤 ò q ò g ò 셤 ò g ò g ö a ç ò

The cellulose synthase can be used for the improvement of stalk quality for improved stand or slage. It also provides an increased concentration of cellulose in the pericarp, hardening the kernel and improving its handling ability. The sequences are used to produce transgenic plants and seeds expressing the cellulose synthase. The polynucleotide is used for modulating, preferably increasing, the level of the synthase in a plant cell. The plants are preferably monocots. The polynucleotide is also used as a probe or primer in the detection quantitation or isolation of gene transcripts. The probes are useful in detecting defictencies in the level of monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants of the gene, for monitoring upregulation of for the set as molecular markers in plant breeding programs. The gene, for the set as molecular markers in plant breeding programs. The probates as molecular markers in plant programs. isolated nucleic acids of the present invention or also be used for recombinant expression of their encoded polypeptides or for use as immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.

1077 AA; Sequence

5 Gaps 93.7%; Score 5415.5; DB 21; Length 1077; 92.3%; Pred. No. 0; 46; Mismatches Conservative Similarity Best Local Sim Matches 997; Query Match

9 1 MDGDADALKSGRHGAGDVCQICADGLGTTLDGDVFTACDVCRFPVCRPCYEHERKEGTQA

9

CLQCKTKYKRHRGSPAIRGEEGDDTDADDGSDFNYPASGTEDQKQKIADRMRSWRMNTGG 120 61 QQ

à

g

SGNVGHPKYDSGEIGLSKYDSGEIPRGYVPSVTNSOMSGEIPGASPDHHMMSPTGNISRR

APFPYVNHSPNPSREFSGSIGNVAWKERVDGWKMKQDKGAIPMTNGTSIAPSEGRAATDI 119 181 8 ò

g

DASTEYNMEDALLNDETROPLSRKVPIASSKINPYRMVIVLRLVVLSIFLHYRLTNPVRN 241 q ò

AYPLWLLSVICEIWFALSWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVS 301 ò

588 g

TVDPLKEPPIVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFDALAETSEFARKWVPFV 420 359 361 g à

KKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVSKALKVPEE 419 421 g à

GWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAG 481 a ò

900 AMNALVRVSAVLTNGQYMLNLDCDHY INNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDG ò

IDRNDRYANRNIVFFDINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKKPGFLASL 539 601 g ŏ

CGGKKRASKSKKRSSDKKKSNKHVDSSVPVFNLEDIEEGVEGAGFDDEKSVLMSQMSLEK 720 661

IDRNDRYANRNTVFFDINLRGLDGIQGPVYVGTGCVFNRTALYGYEPPIKQKKGGFLSSL

SDEDGDFAELYMFKWTTLIPPTTILIINLVGVVAGISYAINSGYQSWGPLFGKLFFAFW 1017 VIVHLYPFLKGLMGRONRTPTIVIVWAVLLASIFSLLWVRVDPFTTRLAGPNIQTCGINC 1080 960 777 957 CGGRKKASKSKK-GSDKKKSQKHVDSSVPVFNLEDIEEGVEGAGFDDEKSLLMSQMSLEK 717 YGGRLKFLERFAYINTIYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFL ILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYG SIFATGILEMRWSGVGIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKA NDEEGDFAELYMFKWTTLLIPPTTILIINWVGVVAGTSYAINSGYQSWGPLFGKLFFAFW 868 841 629 718 781 901 961 Pp qq δý qq Ω OD Qγ g δλ g οy δ

AAY8411 RESULT

Ā AAY84114 standard; Protein; 1077

AAY84114;

(first entry) 03-JUL-2000 Amino acid sequence of a maize cellulose synthase.

Maize; cellulose synthase; stalk quality; stand; silage; cellulose; transgenic plant; plant breeding marker.

Zea mays.

/note= "encoded by MGG" Location/Qualifiers Misc-difference

WO200009706-A2

24-FEB-2000

99WO-US18760. 16-AUG-1999;

17-AUG-1998;

(PION-) PIONEER HI-BRED INT INC

×

BA,

Bowen

WPI; 2000-224343/19.

Dhugga KS, Helentjaris TG,

N-PSDB; AAZ99512

New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein

Claim 15; Page 142-144; 119pp; English.

The present sequence represents a maize cellulose synthase polypeptide. The cellulose synthase can be used for the improvement of stalk quality for improved stand or silage. It also provides an increased concentration of cellulose in the pericarp, hardening the kernel and improving its handling ability. The sequences are used to produce transgenic plants and seeds expressing the cellulose synthase. The polynucleotide is

used for modulating, preferably increasing, the level of the synthase in a plant cell. The plants are preferably monocots. The polynucleotide is also used as a probe or primer in the detection quantitation or isolation of gene transcripts. The probes are useful in detecting deficiencies in the level of mRNA in screenings for desired transgenic plant, for detecting mutations in the gene, for monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants of the gene, or for use as mollecular markers in plant breeding programs. The isolated nucleic acids of the present invention can also be used for the present invention can also be used for the monocompounds. immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.

1077 AA; Sequence

ñ Gaps Length 1077; Indels DB 21; 34; 93.7%; Score 5415.5; 92.3%; Pred. No. 0; ive 46; Mismatches al Similarity 92.3 997; Conservative Query Match Best Local Matches

9 9 1 MDGDADALKSGRHGAGDVCQICADGLGTTLDGDVFTACDVCRFPVCRPCYEHERKEGTQA 셤

CLQCKTKYKRHRGSPAIRGEEGDDTDADDGSDFNYPASGTEDQKQKIADRMRSWRMNTGG 120 61

> ŏ g ò q ò g ò qq δ ΩD ö qq à 셤 ò g à g ò qq ò g

61

300 DASTEYNMEDALLNDETROPLSRKVPIASSKINPYRMVIVLRLVVLSIFLHYRLTNPVRN 241

239

AMNALVRVSAVLTNGQYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDG

541

900

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718 721 ŏ

ILTGFKMHARGWRSVYCMPKRP YGGRLKFLERFAYINTIYPLT NDEEGDFAELYMFKWTTLLIPP SDEDGDFAELYMFKWTTLLIPP SIFATGILEMRWSGVGIDEWWR SIFATGILEMRWSGVGIDEWWR 901 868 928 781 841 961 q ö g ŏ ద οy d Q

Protein; AAY84119 standard; 03-JUL-2000 AAY84119; RESULT 4 AAY84119

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Location/Qu Maize; cellulose synthase; transgenic plant; plant bre Amino acid sequence of a ma (first entry) Zea mays. Key HID NAME OF A COLOR OF

quality; stand; silage; cellulose;

ellulose synthase

/note= "enc 99WO-US18760 Misc-difference WO200009706-A2 16-AUG-1999; 7-AUG-1998; 24-FEB-2000

(PION-) PIONEER HI-BRED INT Helentjaris TG, WPI; 2000-224343/19. N-PSDB; AAZ99527. Dhugga KS,

New genes which encode maiz useful for modulating the e and to produce transgenic p Claim 15; Page 181-183; 119 The present sequence repres

The cellulose synthase can for improved stand our silag of cellulose in the pericar handling ability. The seque and seeds expressing the ceused for modulating, prefer in a plant cell. The plants is also used as a probe or isolation of gene transcripedeficiencies in the level o

1020 1080 840 900 960 897 APINESDRINQVLRWALGSVEILFSRHCPLWYG /YCILPAICLLTGKFIMPEISNLASIWFIALFL VIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKA INMVGVVAGTSYAINSGYQSWGPLFGKLFFAFW **VLLASIFSLLWVRVDPFTTRLAGPNIQTCGINC**

Wang X; BA, by MGG" ers eu 98US-0096822

lulose synthase polypeptides in plants sion of cellulose synthase in plants expressing the novel protein

nglish.

a maize cellulose synthase polypeptide.
ed for the improvement of stalk quality
also provides an increased concentration
rdening the kernel and improving its
are used to produce transgenic plants se synthase. The polynuclectide is increasing, the level of the synthase preferably monocots. The polynuclectide in the detection quantitation or he probes are useful in detecting a in screenings for desired transgenic

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   monitoring upregulation
         of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants of the gene, or for use as molecular markers in plant breading programs. The isolated nucleic acids of the present invention can also be used for recombinant expression of their encoded polypeptides or for use as immunosens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.
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                                                                                                                                                                DB 21; Length 1043;
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                                                                                                                                                                91.0%; Score 5255.5; 92.6%; Pred. No. 0;
                                                                                                                                                                                        42; Mismatches
plant, for detecting mutations in the
                                                                                                                                                                            Best_Local Similarity 92.6
Matches 969; Conservative
                                                                                                                                        1043 AA;
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ILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYG

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The present sequence represents a maize cellulose synthase polypeptide.

The cellulose synthase can be used for the improvement of stalk quality
for improved stand or slage. It also provides an increased concentration
of cellulose in the pericarp, hardening the kernel and improving its
handling ability. The sequences are used to produce transgenic plants
and seeds expressing the cellulose synthase. The polynucleotide is
used for modulating, preferably increasing, the level of the synthase
in a plant cell. The plants are preferably monocots. The polynucleotide
is also used as a probe or primer in the detection quantitation or
isolation of gene transcripts. The probes are useful in detecting
deficiencies in the level of mRNA in screenings for desired transgenic
plant, for detecting mutations in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection a markers in plant breeding programs. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maize; cellulose synthase; stalk quality; stand; silage; cellulose; transgenic plant; plant breeding marker.
SIFATGILEMRWSGVGIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New genes which encode maize cellulose synthase polypeptides in useful for modulating the expression of cellulose synthase in pland to produce transgenic plants expressing the novel protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding a maize cellulose synthase.
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                                                                                                                                                                                                                                                                                                                                               VIVHLYPFLKGLMGRQNRTPTIVIVW 1046
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CC Trecombinant expression of their encoded polypeptides or for use as continuogens in the perparation and/or screening of entitlodies. The proceins con the employed in assays for enzyme agonists or antigonists of the proceins con the employed in assays for enzyme agonists or antigonists. The proceins con the employed in assays for enzyme agonists or antigonists of the proceins con the employed in assays for enzyme agonists or antigonists. The proceins con the employed in assays for enzyme agonists or antigonists of the proceins of the	Db 896 ISIFATGILEMRASGVGI Qy 960 ANDEGCDFAELYMFKWTT Db 956 ATDEGCDFAELYMFKWTT Qy 1020 WVIVHLYPFLKGLMGRQN Qy 1020 WVIVHLYPFLKGLMGRQN Qy 1080 C 1080 Db 1076 C 1076	RESULT 6 AAG48734 ID AAG48734 standard; Prot XX AC AAG48734; XX DT 18-OCT-2000 (first ent XX DY Arabidopsis thaliana pr XX KW Protein identification; KW hybridisation assay; ge KW hybridisation assay; ge XX	8		11 MAY - 1999; 14 MAY - 1999; 14 MAY - 1999; 14 MAY - 1999; 14 MAY - 1999; 18 MAY - 1999; 20 MAY - 1999; 21 MAY - 1999; 24 MAY - 1999; 25 MAY - 1999; 27 MAY - 1999; 28 MAY - 1999;
recombinant expression of their encoded polypeptides or for use as immunogens to antipodies. The proteins can be employed in assays for enzyme agonists or antipodies. The proteins can be employed in assays for enzyme agonists or antigens to obtain antipodies specifically immunoractive with a protein. Sequence 1006 AA; Ouery Match Best Local Similarity 89.0%, Score 5143; DB 21; Length 1076; Best Local Similarity 87.0%; Page 100.0%; Mismatches 59; Indeis 6; Ca Matcher 841; Conservative 69; Mismatches 59; Indeis 6; Ca Matcher 841; Conservative 100.0%; Mismatches 59; Indeis 6; Ca Matcher 841; Conservative 100.0%; Mismatches 59; Indeis 6; Ca Matcher 841; Conservative Mismatches 59; Indeis 6; Ca Matcher 841; Conservative Mismatches 59; Indeis 6; Ca Matcher 100.0%; Mismatches 1	.,0				
. א פ א פ א פ א ע א ע א ע א ע א ע א ע א א א א	recombinant expression of their encoded polypeptides or for use as immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagoni of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein. Sequence 1076 AA; Sequence 1076 AA; B9.0%; Score 5143; DB 21; Length 1076; aest Local Similarity 87.6%; Pred. No. 0; 4atches 947; Conservative 69; Mismatches 59; Indels 6; Ga atches 947; Conservative 11 1 1 1 1 1 1 1 1 1	61 CLOCKTKYKRHRGSPAIRGEEGDDTDADDGSDENTPAGGTEDOKQKIADRARSHRANTGG 61 CLOCKTKYKRHRGSPAIRGEEGDDTDADDGSDENTPAGGTEDOKQKIADRARSHRANTGG 60 CPOCKTKYKRHRGSPPYHGENEDVDADDVSDYNYQASGNODOKQKIAERALTWITNSRG 121 SGNVGHPKYDSGEIGLSKYDSGEIPRGYVPSYTNSQMSGEIPGASPDHHMMSPTGNISRR 61 ::	300 NAYPLWLLSVICEINFALSWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAUDIFV	540 GAMNALVRVSAVLINGQYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRFD	720 KREGOSAAFVASTLMEYGGVPOSSTPESLLKEAIHVISCGYEDKSEWGTEIGWIYGSVTE

05-AUG-1999; 05-AUG-1999; 06-AUG-1999;	09-AUG-1999;	09-AUG-1999;	10-AUG-1999;	12-AUG-1999;	13-AUG-1999;	13-AUG-1999;	17-AUG-1999;	18-AUG-1999;	20-AUG-1999;	20-AUG-1999;	23-AUG-1999;	23-AUG-1999;	25-AUG-1999;	27-AUG-1999;	27-AUG-1999;	27-AUG-1999;	31-AUG-1999;	01-SEP-1999;	07-SEP-1999;	10-SEP-1999;	15-SEP-1999;	16-SEP-1999;	20-SEP-1999;	22-SEP-1999;	23-SEP-1999; 24-SEP-1999;	28-SEP-1999;	29-SEP-1999;	04-0CT-1999;	06-0CT-1999;	07-OCT-1999;	12-0CT-1999;	13-0CT-1999;	13-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-OCT-1999;	14-0CT-1999;	18-OCT-1999;	21-OCT-1999;	21-0CT-1999;	21-OCT-1999;	21-OCT-1999;	22-OCT-1999;	22-0CT-1999;	22-OCT-1999;	25-OCT-1999;	25-0CT-1999;	26-OCT-1999;	26-0CT-1999;	26-OCT-1999; 28-OCT-1999;	28-OCT-1999;	28-OCT-1999;
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03-JUN-1999; 03-JUN-1999; 04-JUN-1999; 04-JUN-1999;	-NOC- 70 -NOC- 80	10-JUN-	- NOD-01	16-JUN	16-JUN-	19-11N-	18-JUN-	18-JUN.	18-JUN.	NDD-81	18-JUN.	18-JUN	NOD-8T	18-JUN	18-JUN	21 - JUN	23 - JUN-	23 - JUN	24 -JUN	NDD-87	30-JUN-	01-JUL	01-JUL	02-JUL	-105-80 -101-80	09-JUL	12-JUL	13-JUL- 14-JUL-	15-JUL	16-JUL	19-JUL-	19-JUL	19-JUL 19-JUL	19-JUL	19-JUL	20-JUL- 20-JUL-	20-JUL	21-JUL	21-JUL 21-JUL	22-JUL	22-JUL	22-JUL 22-JUL	23-JUL	23-JUL	23-JUL	27-701.	27 - JUL.	27-JUL	28-JUL	02-AUG	02-AUG	03-AUG
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ransduction pathway; metabolic pathway; oping; gene expression control; promoter;

Igment SEQ ID NO: 61573.

M Be	Query Match 78.4%; Score 4530; DB 21; Length 1054; Best Local Similarity 78.6%; Pred. No. 0; Matches 839; Conservative 98; Mismatches 104; Indels 26; Gaps 8;	QQ	 1008 GRQNRTPT		ASIES
% g	19 COICADGLGTTLDGDVFTACDVCRFPVCRPCYBHERKEGTQACLQCKTKYKRHRGSPAIR 78	RESULT 7 AAG48733 ID AAG4	18733 s	tandard; Prot	tein;
χ̈́	79 GEEGDDTDADDGS-DFNYPASGTEDQKQKIADRMRSWRMNTGGSGNVGHPKYDSGEIGLS 137	X Y X	AAG48733;		
ą	69 GDKDEDGLADEGTVEFNYPQKEKISERMLGWHLTRGKGEEMGEPQYDK 116	i i i	18-OCT-2000	(first en	entry)
ζ		XOE	Arabidopsis t	thaliana p	0
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à á	256 ETRQPLSRKVPIASSKINPYRMVIVLRLVVLSIFLHYRLTNPVRNAYPLMLLSVICEIWF 315 : :	X X X Q	EP1033405-A2.		
à	ALSWILDOFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPLKEPPIVTANT	P.Y.	25-FEB-2000;	2000EP-0301	0143
g	288 ALSWILDQPPKWFPVNRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPLKEPPLVTANT 347	X X X	25-FEB-1999; 05-MAR-1999;		2182
Š Š	376 VLSILAVDYPVDKVSCYVSDDGASMLTFDALAETSBFARKWVPFVKKYDIBPRAPEFYFC 435 3.0 VLSTLAVDYPVDKVSCYVSDDASAKLEPDALAETSBFARKWVPFVKKYDIBPRAPEFYFC 435 3.0 VLSTLAVDYPVDVOVYSCYVSTANA VLSTPARKAVDSAVEVARVANA VOT	7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	09-MAR-1999; 23-MAR-1999; 25-WAR-1999;		23546 25786
3 8	OKIDYIKDKVOPSEVKDRRAMKEYEEFKIRINALVSKALKVPEEGMIMODGTPWPGN 4	ያ ያ ያ	29-MAR-1999; 01-APR-1999;		2678
· 6		P. P	06-APR-1999; 08-APR-1999;		2823
δ	RDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFOHHKKAGAMNALVRVSAVLTNG	R R G I	16-APR-1999; 19-APR-1999; 21-APR-1999;		3007
요 .	RDHPGMIQVFLGQNGGLDAEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNG 52	ማ ያ ማ ያ	23-APR-1999; 23-APR-1999;		3051
δ O	556 QYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFF 615 ::	8 8 9 6 6	28-APR-1999; 30-APR-1999; 30-APR-1999;		3240
y g	616 DINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKRPGFLASLCGGKKASKSKKR 673 	7. 07 07 7. 07 07 07 7. 07 07 07	04-MAI-1999; 05-MAY-1999; 06-MAY-1999; 06-MAY-1999;		3248
λ	SSDKKKSNKHVDSSVPVFNLEDIEEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFVASTL	7 7 7 Y	07-MAY-1999; 11-MAY-1999; 14-MAY-1999;		3286 3425 3421
අ	ESDKKKSGRHTDSTVPVFNLDDIEEGVEGAGFDDEKALLMSQMSLEKRFGQSAVFVASTL	ሟ ሟ	14-MAY-1999; 14-MAY-1999;		3421
à á	/34 MEYGGVPQSSTPESLLKEALHVISCGXEDKSEMGTEIGWITGSVTEDLLTGFKMHAKGWR /93 /	ች ያ ያ ያ አ አ አ ያ	14 -MAY -1999; 18-MAY -1999; 19-MAY -1999; 20-MAY -1999;		3476
oy ob	794 SYYCMPKRPAFKGSAPINLSDRLNOYLRWALGSYEILFSRHCPLMYGYGGRLKFLERFAY 853 -	PR PR	21-MAY-1999; 24-MAY-1999; 25-MAY-1999;		3535
S G	854 INTTIYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWS 913 	PR PR PR	27-MAY-1999; 28-MAY-1999; 01-JUN-1999; 03-JUN-1999;	990S-013639 990S-013678 990S-013722 990S-013752	3678
Qy Dp	914 GVGIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMF 973 	PR PR PR	04-JUN-1999; 07-JUN-1999; 08-JUN-1999; 10-JUN-1999;		3772
Qy Dp	974 KWTTLLIPPTTLLINWVGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLM 1033 	ያ ያ ያ ያ ያ አ ያ ያ ያ ያ	14-JUN-1999; 16-JUN-1999; 16-JUN-1999; 16-JUN-1999;		3945
οy	1034 GRQNRTPTIVIVWAVLLASIFSLLWVRVDPFTTRLAGPNIGTCGINC 1080	7 Y R	18-JUN-1999;	990S-01	300

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KYDSGEIPRGYVPSVTNSO-MSGEIPGASPDHHMMSPTGNISRRAPFPY-VNHSPNPSRE 195
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             |----EVSHNHLPRLTSRQDTSGEFSAASPERLSVSSTIAGGKRLPYSSDVNQSPNRRIV
                                                RDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNG
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ying target proteins ally active compounds, comprising cid or aminon acid sequences from plant sequences from non-plant organisms using e plant sequences having an E-value e E-value of most similar non-plant peptides or nucleic acids encoding them ators. The identified modulators are
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                                         erbicide
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                                         agricult
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                   DINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKA--KKPGFLASLCGGKKKASKSKKR
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           RDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNG
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                                                                                                                                                                                                                                                                                                                                        cellulose synthase; RSW1 protein; beta-1,4-glucan;
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This polypeptide is encoded by cDNA clone Ath-B (see AAV06567)
that was isolated from an Arabidopsis thaliana cDNA library using
pCR primers (see AAV06563-34) based on cellulose synthase RSW1
genomic clone 23H12 (see AAV06563) and EST clone AAT20782 (see
AAV06562). It is closely related to Arabidopsis cellulose synthase RSW1
cprotein (see AAW03561-17). Claimed nucleic acid molecules (see
AAV06562-69) codung for claimed polypeptides (see AAW33816-20 and
AAW46202) involved in cellulose biosynthesis can be used to
manipulate the cellulose and/or beta-glucan content of transgenic
plants. Expression of nucleic acids in the sense orientation
increases the level of cellulose and reduces the level of
non-crystalline beta-14-glucan and starch, providing plants with
corresponding to the content of a transgenic corresponding to the content of a transgenic plant, e.g. to improve digestibility or to
alter carbon partitioning such that increased carbon is available
correction content of a transgenic plant, e.g. to improve digestibility or to
alter carbon partitioning such that increased carbon is available
correction content of a transgenic plant, e.g. to improve digestibility or to
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- useful for manipulation
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A encoding cellulose biosynthetic enzyme cellulose and beta-1,4-glucan
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                                                                                                                                          29; Page 144-149; 207pp; English.
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599 DINLRGLDGIQGPVYVGTGCVFNRTALYGYEPPIKVKHKKPSLLSKLCGGS	# SOUNTROUNTY DOSYFYER NEED LEEGY EGAGE DUEACY LMOGRASLEARE GUSAAFYASIL / 73. : : :	OY 734 MEYGCVPQSSTPESLLKEAIHVISCGYEDKSEMGTEIGWIYGSVTEDILTGFKMHARGWR 793 	QY 794 SVYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAY 853	OY 854 INTTIYPLTSLPLLVYCILPALCLLTGKFIMPBISNLASIWFIALFLSIFATGILEMRWS 913	QY 914 GVGIDEWWRNEGFWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMF 973	Oy 974 KWTTLLIPPTILIINMYGVVAGTSYAINSGYOSWGPLFGKLFFAFWVIVHLYPFLKGLM 1033 	1034 GRQNRTPTIVIVWAVLLASIFSLLWVRVDPFTTRLAGPNIOTCGINC 1080	RESULT 10 AAG48735 standard, Protein; 959 AA. XX C AAG48735; XX XX C AAG48735; XX XX Arabidopsis thaliana protein fragment SEQ ID NO: 61575. XX Arabidopsis thaliana protein fragment SEQ ID NO: 61575. XX Arabidopsis thaliana. XX Arabidopsis thaliana. XX Arabidopsis thaliana. XX XX Arabidopsis thaliana. XX XX XX XX XX XX XX XX XX

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28 - JUL - 1999;
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28 - JUL - 1999;
29 - JUL - 1999;
20 - AUG - 1999;
31 - AUG - 1999;
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23 - AUG - 1999;
26 - AUG - 1999;
26 - AUG - 1999;
27 - AUG - 1999;
27 - AUG - 1999;
30 - AUG - 1999;
31 - AUG - 1999;
11 - SEP - 1999;
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10 - SEP - 1999
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21-OCT-1999;
21-OCT-1999;
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348
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                                                                                                                                                                                                                                                       MMSPTGNISRRAPFPY-VNHSPNPSREFSGSIGNVAWKERVDGWKMKQDKGAIPMTNGTS
                                                                                                                                                                                                                                                                 SVSSTIAGGKRLPYSSDVNQSPNRRIVDPVGLGNVAWKERVDGWKMKQEKNTGPV---ST
                                                                                                                                                                                                                                                                                                                                                                                        PSQLAAVDIFVSTVDPLKEPPIVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFDALAE
                                                                                                                                                                                                                                                                                                                                                                                                                                  TSEFARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALVSKALKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTEIGWIYGSVTEDILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNQVLRWALGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEILFSRHCPLWYGYGGRLKFLERFAYINTTIYPLTSLPLLVYCILPAICLLTGKFIMPE
                                                                                                                                                                 DB 21; Length 959
                                                                                                                                                                                        19;
                                                                                                                                                                                        92; Indels
                                                                                                                                                                 72.9%; Score 4209.5;
80.4%; Pred. No. 0;
ive 80; Mismatches
99US-0160815.
99US-0160980.
99US-0160981.
99US-0161404.
99US-0161405.
99US-0161360.
99US-0161359.
99US-0161361.
99US-0161361.
99US-0161361.
99US-0161363.
                                                                                                                                                                                        Conservative
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20;

Gaps

9

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TTLLIPPTTLLINMVGVVAGTSYAINSGYQSW 1008
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TSLLIPPTTVLVINLVGMVAGISYAINSGYQSW 1001
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                                                                                                                                                                                                                                                       RQPLSRKVPIASSKINPYRMVIVLRLVVLSIFL 290
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                                                                   GSIGNVAWKERVDGWKMKQDKGAIPMTNGTSIA
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KGLNSVDWKERVESWRVKQDKNMLQVTN----
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DDLDNEFNY-----KQ------
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                     Length 1074;
                                             59;
                                             153; Indels
                       21;
                       DB
                     ore 3993.5;
d. No. 0;
Mismatches
                       69.1%;
68.4%;
                                                                                          DGDAPVPAKPTKSANGOVCQIC
                                                                                                                                                                                                                                                                       - KYPEARGDME-GTGSNGEDMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVQFPQREDGIDRNDRYANRH
||||||||||||
YVQFPQRFDGIDLHDRYANRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       949 GIDTNFTVTSKANDEEGDFAEL
                                                                    DGDADA-LKSGRHGAGDVCQIC
                                                                                                                 CLQCKTKYKRHRGSPAIRGEEG
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1074
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881

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The present sequence represents a maize cellulose synthase polypeptide.

The cellulose synthase can be used for the improvement of stalk quality

of callulose in the perioarp, hardening the kernel and improving its

handility. The sequences are used to produce transgenic plants

and seeds expressing the cellulose synthase. The polynucleotide is

used for modulating, preferably increasing, the level of the synthase

in a plant cell. The plants are preferably monocots. The polynucleotide

is also used as a probe or primer in the detection quantitation or

isolation of gene transcripts. The probes are useful in detecting

deficiencies in the level of mRNA in screenings for desired transgenic

plant, for detecting mutations in the gene, for monitoring upregulation

of expression or changes in enzyme activity in screening assays of

compounds, for detection of any number of allelic variants of the gene,

compounds, for detection of any number of allelic variants of the

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proteins of the preparation and/or screening of antibodies. The

proteins of the preparation and/or screening of antibodies. The
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                                                                                                                                                                                                                                                                                                                                                                                                                 Maize; cellulose synthase; stalk quality; stand; silage; cellulose; transgenic plant; plant breeding marker.
of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.
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                                                                                                                                                                                                                                         AAY84112 standard; Protein; 1074 AA.
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GIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINWYGVVAGTSYAINSGYOSW 1008
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                                                                                                                                                                                                       - KYPEARGDME-GTGSNGEDMQWVDDARLPLSRIVPISSNQLNLYRIVIILRLIILCFFF
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         CLQCKTKYKRHRGSPAIRGEEGDDTDADD-GSDFNYPASGTEDQKQKIADRMRSWRMNTG
                                                                                            120 GSGNVGHPKY----DSGEIGLS-KYDSGEIPRGYVPSVTN-SQMSGEIPGASPDHH-MMS
                                                                                                                                             PTGN-ISRRAPFPYVNHSPNPSREF-SGSIGNVAWKERVDGWKMKQDKGAIPMTNGTSIA
                                                                                                                                                                    PTSSYVDPSVPVPV--RIVDPSKDLNSYGLNSVDWKERVESWRVKQDKNMLQVTN----
                                                                                                                                                                                            PSEGRAATDIDASTEYNMEDALLNDETRQPLSRKVPIASSKINPYRMVIVLRLVVLSIFL
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The cellulose synthase can be used for the improvement of stalk quality for improved stand or silege. It also provides an increased concentration of cellulose in the pericarp, hardening the kernel and improving its handling ability. The sequences are used to produce transgenic plants and seeds appreciating the cellulose synthase. The polynucleotide is used for modulating, preferably increasing, the level of the synthase of a plant cell. The plants are preferably monocots. The polynucleotide is used for modulating or primer in the detection quantitation or isolation of gene transcripts. The probes are useful in detecting deficiencies in the level of mRNN in screenings for desired transgenic collar market of monitoring upregulation of expression or changes in enzyme activity in screening assays of compounds, for detection of any number of allelic variants of the gene, continued the compounds in the plant breeding programs. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genes which encode maize cellulose synthase polypeptides in plants useful for modulating the expression of cellulose synthase in plants and to produce transgenic plants expressing the novel protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated nucleic acids of the present invention of his be used for recombinant expression of their encoded polypeptides or for use as immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.
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transgenic plant; plant breeding marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1074;
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                                                                                                                                                                                                                                                                                                            Amino acid sequence of a maize cellulose synthase.
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bred. No. 0;
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1066 TRLAGPNIQTCGINC 1080
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WINYPITSVPLIAYCVLPAICLLTNKFIIPEIS 881 DD-GSDFNYPASGTEDQKQKIADRMRSWRMNTG 119 ---PHHRIPRLTSGQQISGEIPDASPDRHSIRS LINVDCDHYFNSSKALREAMCFWMDPALGRKTC ROPLSRKVPIASSKINPYRMVIVLRLVVLSIFL || ::||| |DDLDNEFNY-----KQ-227 -KYPEARGDME-GIGSNGEDMC 405 EFARKWVPFCKKHNIEPRAPE VSKALKVPEEGWIMQDGTPWPG CLOCKTKYKRHRGSPAIRGEEG CPQCKTRYKRQKGSPRVHGDD 120 GSGNVGHPKY----DSGEIGLS -- GNGKGPEWOLQGDDADLSSS 173 PTGN-ISRRAPFPYVNHSPNP 174 PTSSYVDPSVPVPV--RIVDPS **PSEGRAATDIDASTEYNMEDAI** HYRLTNPVRNAYPLWLLSVICE **EFARKWVPFVKKYDIEPRAPE** VAKAQKVPEEGWTMADGTAWP 942 GIDTNFTVTSKASDEDGDFAE **QLAAVDIFVSTVDPLKEPPIV** 591 YVQFPQRFDGIDRNDRYANRN AK -- KPGFLASLCGGKKKASK KSVLMSQMSLEKRFGQSAAFV SVLMSQRKLEKRFGQSPIFI EIGWIYGSVTEDILTGFKMHA 829 ILFSRHCPLWYGYGGRLKFLE 889 NLASIWFIALFLSIFATGILE GIDTNFTVTSKANDEEGDFAE PGFQHHKKAGAMNALVRVSAV GPLFGKLFFAFWVIVHLYPFL 1066 TRLAGPNIQTCGINC 1080 CKAAA--LGQCGVNC 1074 1062 g

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The cellulose synthase can be used for the improvement of stalk quality
of cellulose stand or slage. It also provides an increased concentration
of cellulose in the pericarp, hardening the kernel and improving its
handling ability. The sequences are used to produce transgenic plants
and seeds expressing the cellulose synthase. The polynuclectide is
used for modulating, preferably increasing, the level of the synthase
in a plant cell. The plants are preferably monocots. The polynuclectide
is also used as a probe or primer in the detection quantitation or
isolation of gene transcripts. The probes are useful in detecting
deficiencies in the level of mRNA in screenings for desired transgenic
plant, for detecting mutations in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection of any number of allelic variants of the gene,
compounds, for detection of any number of allelic variants of the gene,
compounds for detection of the present invention can also be used for
recombinant expression of the present invention can also be used so
immunorate in the present invention can also be used for
immunorate in the present in a proper level or for use as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes which encode maize cellulose synthase polypeptides in plants ful for modulating the expression of cellulose synthase in plants to produce transgenic plants expressing the novel protein -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| : | : | |||||| | | : |||||| || || DGDVPGSAKPIKSANGQVCQICGDSVGVSATGDVFVACNECAFPVCRPCYEYERKEGNQC 82
                                                                                                                                 cellulose synthase; stalk quality; stand; silage; cellulose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.
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                                                                                                       Amino acid sequence of a maize cellulose synthase.
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Pred. No. 0;
                                                                                                                                               ransgenic plant; plant breeding marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 102-105; 119pp; English.
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245
                        AAY84109 standard; Protein; 1075
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68.5%;
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                                                                               (first entry)
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les 747; Conserv
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FTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINMVGVVAGTSYAINSGYQSWGPLFG 1013
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                                                                             236 AATDIDASTEYNMEDALLNDETRQPLSRKVPIASSKINPYRMVIVLRLVVLSIFLHYRLT
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The cellulose synthase can be used for the improvement of stalk quality
for improved stand or silage. It also provides an increased concentration
of cellulose in the pericarp, hardening the kernel and improving its
nd seeds expressing the cellulose synthase. The polynucleotide is
used for modulating, preferably increasing, the level of the synthase
or used for modulating preferably monocots. The polynucleotide
is also used as a probe or primer in the detection quantitation or
solation of gene transcripts. The probes are useful in detecting
of esticiencies in the level of manA in screenings for desired transgenic
plant, for detecting mutations in the gene, for monitoring upregulation
of expression or changes in enzyme activity in screening assays of
compounds, for detection of any number of allelic variants of the gene,
or for use as molecular markers in plant breeding programs. The
confoundinant expression of the present invention can also be used for
tecombinant expression of the present invention can also be used sof imminioned the present invention and also the present invention and and the present invention and the present invention and the present invention and also be used sof imminioned the present invention of antibodies when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogens in the preparation and/or screening of antibodies. The proteins can be employed in assays for enzyme agonists or antagonists of enzyme function or for use of immunogens or antigens to obtain antibodies specifically immunoreactive with a protein.
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                                                                                                                                                                                                                 Maize; cellulose synthase; stalk quality; stand; silage; cellulose;
transgenic plant; plant breeding marker.
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68.5%; Pred. No. 0;
iive 132; Mismatches 163;
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                                                                                                                       (first entry)
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N-PSDB; AAZ99515.
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Misc-difference 245
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AAY84115
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PPTTILIINMVGVVAGTSYAINSGYQSWGPLFG 1013 TIVIVWAVLLASIFSLLWVRVDPF---TTRLAG 1070 |||||||::|||||||||||::||| TIVIVWSILLASIFSLLWVKIDPFISPTQKAAA 1067 | |||:|::| ||:||:||:|| | ||:: RIVPISSNQLNLYRVVIILRLIILCFFFQYRVS 290 DKVQPSFVKDRRAMKREYEEFKIRINALVSKAL 475 **QSSTPESLLKEAIHVISCGYEDKSEWGTEIGWI 773** GYVPSVTN-SQMSGEIPGASPDHH-MMSPTGN-IRIPRLTSGQQISGEIPDASPDRHSIRSPTSSY AWKERVDGWKMKQDKGAIPMTNGTSIAPSEGR KVPIASSKINPYRMVIVLRLVVLSIFLHYRLT **QFPKWFPINRETYLDRLALRYDREGEPSQLAAV** DYPVDKVSCYVSDDGASMLTFDALAETSEFARK OVFLCHSGGLDTEGNELPRLVYVSREKRPGFQH CDHYINNSKAVREAMCFLMDPNLGPQVCYVQFP CDHYFNSSKALREAMCFMMDPALGRKTCYVQFP DGIQGPVYVGTGCVFNRTAIYGYEPPIKAK--K NKHVDSSVPVFNLEDIEEGVEGAGFDDEKSVLM RPAFKGSAPINLSDRLNQVLRWALGSVEILFSR LTSLPLLVYCILPAICLLTGKFIMPEISNLASI VRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTN ---KQ---DELDNEFNY ----16:35:09 120 GSGNVGHPKYDSGEIGLSKYDS 120 GSGKGPEWQLQGDDADLSSSAR 177 ISRRAPFPYVNHSPNPSREF-S 179 VDPSVPVPV--RIVDPSKDLNS 356 DIFVSTVDPLKEPPIVTANTVL 411 WVPFCKKHNIEPRAPEFYFAOK SOMSLEKRFGQSAAFVASTLME 233 GG-DME-GTGSNGEXMQMVDDA NPVRNAYPLWLLSVICEIWFAL KVPEEGWIMODGTPWPGNNTRD PGFLASLCGGKKKASKSKKRSS PNIVIKSCCGRRK-KKNKSYMD 83 CPQCKTRYKRQKGSPRVHGDE-236 AATDIDASTEYNMEDALLNDET 416 WVPFVKKYDIEPRAPEFYFCQK HKKAGAMNALVRVSAVLTNGQY **ORFDGIDRNDRYANRNTVFFDI** YGSVTEDILIGFKMHARGWRSV FTVTSKANDEEGDFAELYMFKW WFIALFLSIFATGILEMRWSGV 1014 KLFFAFWVIVHLYPFLKGLMGR HCPLWYGYGGRLKFLERFAYI HCPIWYGYNGRLKLLERLAYIN Search completed: February 19, Job time: 49 secs 1071 PNIQTCGINC 1080 --LGQCGVNC 1075 651 536 774 954 476

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1 MDGDADALKSGRHGAGDVCQ......VDPFTTRLAGPNIQTCGINC 1080
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847 794

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probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana (mouse-ear cress) [C.) Species: Arabidopsis thaliana (mouse-ear cress) [C.) Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 [C.) Accession: F84649 [A. F. Founsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente Nature 402, 751-768, 1999 [A. Filler: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10617197 [A. Founslein and A. Februs preliminary A. Molecule type: DNA A; Residues: 1-1065 [A. Founslein and A. Februs and
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                                                                                 N'Alternate names: protein T1086_80
C'Species: Arabidopsis thallana (mouse-ear cress)
C'Species: Arabidopsis thallana (mouse-ear cress)
C'Sator S: Arabidopsis thallana (mouse-ear cress)
C'Sator S: Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Nakenence number: 225394
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A; Status: preliminary
A; Status: Draft Signal Sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 5
A;Introns: 25/3; 91/1; 184/1; 215/2; 304/2; 419/3; 507/3; 578/3; 650/1; 715/3; 833/3
A;Note: T10B6_80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
                               ellulose synthase catalytic subunit (IRX3) - Arabidopsis thaliana;Alternate names: protein T1086_80;Species: Arabidopsis thaliana (mouse-ear cress);Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000;Accession: T51579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IWFALSWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPLKEPPIVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.8%; Score 3801; DB 2; Length 1026; Best Local Similarity 67.6%; Pred. No. 2.4e-270; Matches 725; Conservative 104; Mismatches 156; Indels 88
                                                           cellulose synthase
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Gaps 61 75

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Indels

Length 1065;

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161

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	348 EPSGLAAVDIEVSTVDPLKEPPIVTANITVLSILAVDYPVDKVSCYVSDDGASMLTFDALA 407 111111 1 :1 :	A; Acc A; Sta A; Mol A; Res A; Cro A; Cro A; Gen A; Gen	A; Accession: T09014 A; Status: translated from GB/EMB: A; Molecule type: mRNA A; Residues: 1-1084 <ari> A; Cross-references: EMBL: AF02717 A; Experimental source: cultivar C; Genetics: ATSP: T22F8. 250; Ath-A</ari>	J D:g2827140; PIDN:AAC39335.1; PID:g2827141 bla
8 8 8	NALVSKALKVPEEGWINQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVSR	A; Map A; Int C; Key	position: 4 rons: 27/3; 156/3; 191/1; 2 words: cell wall synthesis;	343/2; 458/3; 504/3; 546/3; 617/3; 708/1; 773/3 osyltransferase; hexosyltransferase
g v	NILVAKAQKIPEDGWTMEDGTSWPGNNPKDHPGMIQVFLGHSGGLDTDGNELPKLIIVSK EKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHVINNSKAVREAMCFLMDPNLGP 	Que Bes Mat	Query Match 63.5%; Best Local Similarity 62.4%; Matches 687; Conservative 1	ore 3666.5; DB 2; Length 1084; id. No. 1.9e-260; M.smatches 191; Indels 59; Gaps 16;
g Ko	EKRYGEÜHHKKAGAMNALIKVSAVLINGAYLLINGDITENNSKAIKEAMGEMNDFALGA QVCXVQEPQREDGIDRNDRYANRNTVEFDINLRGLDGIQGPVYVGTGCVFNRTALYGYEP :	QY	1 MDGDADA-LKSGRHGAGDVCQI :: :: 20 INADESARIRSVQELSGQTCQI	GTTLDGDVFTACDVCRFPVCRPCYEHERKEGTQ 59
g &	5/4 RCCIVQEPQREDGIDEHDRYANRNIVFEDINLERGEDGIQGEVIVGIGCCERRQALIGIDE 033 648 PIKAKKPGFLASLCGGKKKASKSKK-RSSDKKKSNKHVDSSVPVFNLEDIEEGVEGAG 704 1	Oy Dp	60 ACLOCKTKYKRHRGSPAIRGEB 11	DADDGSDFNYPASGTEDQKQKIADRMRSWRMNTG 119
8 & f	FULEEDLEFILITYNSCEOSARNONSKALTNIEDNASIRKADSNYTLENMELIDEDYE-G FODEKSVLMSQMSLEKREGOSAAFVASTLMEYGGVPQSSTPESLLKEAIHVISGGYEDKS :: : -	oy oy	120 GSGNVGHPKYDSGEIGLSKYDE H H 136 RGGLDSAP	RGYVPSVTNSQMSGEIPGASPDHHMMSPTGNI 177
3 6 6	S EWGTEIGWIYGGWIEBENFGGGFYFITANIFRAGGGEFFIIW EIEBENFRITSCOLEAN. S EWGTEIGWIYGSVTEDILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNGVLRWALL	oy Oy	178 SRRAPFPYVNHSPNDS 177 NRVYPAPFTDSSAPPQARSMVE	REFSGSIGNVAWKERVDGWKMKQ-DKGAIPWING 226 : : : : EFGYGSVAWKDRWEVWKRRQGEKLQVIKHEG 234
g & i	GSVEILESRHCPLWYGYGGRLKFPRYINTTIYPLTSLPLLVYCILPAICLTGKFIM	Qy Db	227 TSIAPSEGRAATDIDASTEYNN 227 :	LNDETROPLSRKVPIASSKINPYRMVIVLRLVVL 286 : : : : : MMDEGROPLSRKLPIRSSRINPYRMLILCRLAIL 287
g & g		QY Db	287 SIFLHYRLTNPVRNAYPLWLLS : : : : 288 GLFFHYRLLHPVNDAYGLWLTE	LWFALSWILDQFPKWPPINRETYLDRLALRYDRE 346 :
8 6		QY	347 GEPSQLAAVDIEVSTVDPLKEI : : 348 GKPSGLAPVDVEVSTVDPLKE	ANTVLSILAVDYPVDKVSCYVSDDGASMLTFDAL 406
	YORWGDLFGKLFFAFWVIVHLYPFLKGLMGRQNRTPTIVIUWAVLLASIFSLLWYRVDPF 106	Qy	407 AETSEFARKWVPEVKKYDIEPP ::::!!	YFCQKIDYLKDKVQPSFVKDRRAMKREYEBFKIR 466 : : :
		QY	467 INALVSKALKVPEEGWIMQDG 	NNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVS 526
Db 1	1052VSTTGV 1057	O.y D.b	527 REKRPGFOHHKKAGAMNALVR 528 REKRPGFDHHKKAGAMNSLIR	TNGGYMLNLDCDHYINNSKAVREAMCFLMDPNLG 586
T085E cellu N;Alt C;Spe	n - Arabidopsis thaliana ss)	Qy Db	587 PQVCYVQFPQRFDGIDRNDRY :	VFFDINLRGLDGIGGPVYVGTGCVFNRTAIYGYE 646
C;Dat C;Acc R;Bev submi		Qy	647 PPIKAKKPGFLASL 	KASKSKRRSSDKKKSNKHVDSSVPVFNLEDIEBG 699 : : : KKSKTKAKDKKTNTKETSKQIHALENVDEG 703
A; Rei A; Acc A; Mol A; Res		QY	700 VEGAGFDDEKSVLMSQMSLEK : : 704 VIVPVSNVEKRSEATQLKLEK	AAFVASTLMEYGGVPQSSTPESLLKEAIHVISCG 759 ::: ::: PVFVASAVLQNGGVPRNASPACLLREAIQVISCG 763
A; Exp R; Exp R; Ari Scien	22F8.250 8 W.; Herth,	Oy Dp	760 YEDKSEWGTEIGWIYGSVTED :	KMHARGWRSVYCMPKRPAFKGSAPINLSDRLNQV 819
A;Tit A;Ref	le: Molecular analysis of cellulose biosynthesis in Arabidopsis. [erence number: 213745; MUID:98111412; PMID:9445479	Oy	820 LRWALGSVEILFSRHCPLWYG	KFLERFAYINTIYPLTSLPLLVYCILPAICLLT 879

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15;
                                                                                                                                                                                                                                                                                                                                    cellulose synthase [imported] - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Bacies: Arabidopsis thaliana (mouse-ear cress)
C;Bacies: 0-oct-2000 #sequence_revision 20-oct-2000 #text_change 20-oct-2000
C;Accession: T52028
R;Joshi, C.
submitted to the EMBL Data Library, May 1998
A;Reference number: 225890
A;Reference number: 225890
A;Accession: T52028
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Golecule type: mRNA
A;Residues: 1-1081 <0055>
A;Residues: 1-1081 <0055>
A;Cross-references: EMBL:AF062485; PIDN:AAC29067.1
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                                                            AINSGYOSWGPLFGKLFFAFWVIVHLYPFLKGLMGRQNRTPTIVIVWAVLLASIFSLLWV
                                                                                                                                                                                      1 MDGDADA-LKSGRHGAGDVCQICADGLGTTLDGDVFTACDVCRFPVCRPCYEHERKEGTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 VLRLVVLSIFLHYRLTNPVRNAYPLMLLSVICEIWFALSWILDQFPKWFPINRETYLDRL
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GKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVGIDEWWRNEQFWVIGGISAHLFAV
                                                                                                         FQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINMVGVVAGTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.0%; Score 3583; DB 2; Length 1 Best Local Similarity 61.0%; Pred. No. 2.6e-254; Matches 676; Conservative 162; Mismatches 198; Indels
                                                                                                                                                                                                                                 RVDPFTTRLAGPNIQTCGINC 1080
                                                                                                                                                                                                                                                   1063 RVNPFVAK-GGPVLEICGLNC 1082
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probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: H84604
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Croin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailon, euss, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venteu, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84604
A;Stelluniany
A;Molecule type: DNA
A;Residues: 1-1088 <STO>
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                                                                                                LMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFFDINLRGLDGIQGPVYVGTGCVFNR
                                                                                                                TAIYGYEPPIKAKKPGFLAS------LCGGKKKASKSKKRSSDKKKSNKHVDSSVPVFN
                                                                                                                                                                                                                                 LEDIEEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFVASTLMEYGGVPQSSTPESLLKEA
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|LENIEEGGRGHKVLNVEQSTEAMQMKLQKKYGQSPVFVASARLENGGMARNASPACLLKEA
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                                                                                                                                                                                                                                                                                                                PAICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVGIDEWWRNEQFWVIGGI
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                                                 Ouery Match 61.9%; Score 3579; DB 2; Length 1088; Best Local Similarity 61.1%; Pred. No. 5.1e-254; Matches 677; Conservative 156; Mismatches 199; Indels 76;
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1054 ILTLLWVRVNPFVAK-GGPILEICGLDC 1080
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A; Map position: 2
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CKTKYKRHRGSPAIRGEEGDDTDADD-----GSDFNYPASGTEDQKQKIADRMRSWRMN 117

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ost, W.E.; Delmer, D.P.; Stalker, D.M. 137-12642, 1996 igs of the bacterial celA genes encoding the 7296; PMID:8901635 91706955; PIDN:AAB37766.1; PID:g1706956 15-2; fiber cotton) n 16-Jul-1999 #text_change 21-Jul-2000 QKIADRMRSWRMNTGGSGNVG-HPKYDSGEIGL 136 TT-----KVEREAEIPPEQOMEDKPAPDA 154 VVLSIFLHYRLTNPVRNAYPLWLLSVICEIWFA 316 OVGRDVCYVOFPORFDGIDRSDRYANRNTVFFD 513 AGFDD-EKSVLMSQMSLEKRFGQSAAFVASTLME 735 ASPDHHMMSPTGNISRRAPFPYVNHSPNPSREF 196 ITNGTSIAPSEGRAATDIDASTEYNMEDALLNDE 256 KIRINALVSKALKVPEEGWIMQDGTPWPGNNTR 496 YVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQ 556 GYGPPSMPSFPKSSSSCSCCCPGKKEPKDPSE 573 VCRPCYEHERKEGTQACLQCKTKYKRHRGSPAI 77 :|: |:|:: ||| :||||:| ICKSCFEYDLKEGRKACLRC------GSPY-TMAA-----HLNKSQDVGIHARHIS---SV GYEPPIKAKKPGFLASLCGGKKKASKSKKRSSD DREGEPSQLAAVDIFVSTVDPLKEPPIVTANTV DALAETSEFARKWVPFVKKYDIEPRAPEFYFCQ NLGPQVCYVQFPQRFDGIDRNDRYANRUTVFFD tic chain celal - upland cotton Length 974; re 3477; DB 2; Length 9; d. No. 1.3e-246; Mismatches 176; Indels sis of cellulose GB/EMBL/DDBJ cellulose synthase (EC 2.4.1.-)
cellulose incomplete (EC 2.4.1.-)
C.Species: Gossyptum hirsutum (u
C.Date: 16-Jul-1999 #sequence_re
C.Accession: T10797
R:Pear, U.R.; Kawaqoe, Y.; Schre
Proc. Natl. Acad. Sci. U.S.A. 93
A;Title: Higher plants contain h
A;Reference number: 217152; MUID
A;Accession: T10797
A;Status: preliminary; translate
A;Molecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule type: mRNA
A;Rolecule cype: AcRes
A;Cross-references: EMBL:U50283;
A;Experimental source: strain Ac
C:Genetics:
A;Gene: celAl
C;Furction: involved in the s
C;Reywords: glycosyltransferase; Query Match 60.2%; Best Local Similarity 61.5%; Matches 657; Conservative 1 18 VCQICADGLGTTLDGDVFTACT AEDNGNSIWKNRVESWKEKKN 8 VCHTCGEHVGLNVNGEPFVACE 78 RGEEGDDTDADDGSDFNYPASC -----DENLLDD-----VEK SKYDSGEIPRGYVPSVTNSOM SGSIGNVAWKERVDGWKMKQDR 214 FSWVLDQFPKWYPVNRETYID : | : :||\ :|: LYRDAKREELDAAIFNLREID TROPLSRKVPIASSKINPYRM S-QPLSTIIPIPKSRLAPYRT LSWILDQFPKWFPINRETYLD LSILAVDYPVDKVSCYVSDDG LSILALDYPVDKVSCYISDDG KKKSNKHVDSSVPVFNLEDIE KIDYLKDKVQPSFVKDRRAMK DHPGMIQVFLGHSGGLDTEGN YMLNLDCDHY INNSKAVREAM INLRGLDGIQGPVYVGTGCVF 514 VNMKGLDGIQGPVYVGTGCVF STLDS----STLDS 59 137 4 197 104 257 155 317 377 274 437 334 497 394 557 454 617 q οy qq οy Q g QQ δy g a δά g οy g q a οŽ οy οy ò à

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callulose synthase (EC 2.4.1.-) catalytic chain cell2 - upland cotton (fragment) (5)pecies: Gossypium hirsutum (upland cotton) (c)Species: Gossypium hirsutum (upland cotton) (c)Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 (c)Accession: T10800 (c)Accessi
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VLSILAVDYPVDKVSCYVSDDGASMLTFDALAETSEFARKWVPFVKKYDIEPRAPEFYFC 435
                                PQDPSEIXKDAKREELDAAIFNLGDLD-----NYDEYDRSMLISQTSFEKTFGLSTVFI
                                                                                                                                                                                                                         RDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNG
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                                                                                                                                                                                                                                                                                                                                    QYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFF
                                                                                                           QKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVSKALKVPEEGWIMQDGTPWPGNNT
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No. 2.5e-198;
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C; Function:
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Cipate: 27-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
Cipate: 27-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
Cipate: 27-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
Ribevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer, A:Reference number: 215387
A:Reference number: 215387
A:Ression: 104870
A:Residues: 1-958 <BEV>
A:Residues: 1-958 <BEV>
A:Residues: 1-958 <BEV>
Cipate: 27-Apr-1999
A:Residues: 1-958 <BEV>
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A:Residues: 1-958 
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                                                                                                              854
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                                                                                                                                            WITLLIPPITILIINMVGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGEEGDDTDADDGSDFNYPASGTEDQKQK1ADRMRSWRMNTGGSGNVGHPKYDSGE1GLS
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                                                                                                                                                                                                                            NTTIYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWSG
                                                                                                                                                                                                                                                                                                                                       VGIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMFK
                                                                                                                 YCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYGY-GGRLKFLERFAYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 4
A;Introns: 60/1; 76/3; 94/1; 149/2; 240/2; 355/3; 40
A;Note: F28A21.190
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIDS
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Genetics: Map position: 1 Query Match Best Local Similarity 42.9%; d. No. 3.4e-161; Matches 488; Conservative 1 Mismatches 256; Indels 214; Gap	YEHEKKEGTQACLQCKTKYKRHR	210 DDPETEBED 133 EIGLSKYDSGEIPRGYVPSVTN ::	193 SREFSGSLGNVAMRENDUGMAR 1 1 1 1 1 1 1 1 1	313 IWFALSWILDQFPKWFPINRET 314		Db 535 RAKKQMEMMAGNNPQETVIV -MSDGSHWPGTWSSGETDNSRGDHAGIIQAMLAP 593 Qy 509 SGGLDTEGNE	Qy 614 FFDINLRGLDGIQGPVYVGTG TAIYGYEPPIKAKKPGFLASLCGGKKKASKSKRR 673 Db 713 FFDVSMRALDGLQGPWYVGTG TALYGFSPPRATEHHGWLGRKKVKISLRR 767 Qy 674 SSDKKRSNKHVDSSVPVF EEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFVA 730 L
Matches 509; Conservative 78; Mismatches 77; Indels 24; Gaps 6; Qy 414 RKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVSK 473	61 ACKFPEGWWQDGTPWPGNNTRDHPGMIOVIGSAGALDVDGKELPRLVYVSREKRPGY 534 QHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVO 111111111111111111111111111111111111	PPIKAKK : : PPVSEKR SVPVFNL	241 PKMTCDCWPSWCCCCGGSRKKSKKGEKKGLLGGLLYGKKMMGKNYVKKGSAPVFDL 694 EDIEEGVEGAGFDD-EKSVLMSQMSLEKRFGQSAAFVASTLMEYGGVPQSSTPESLLKEA 1:1111:1 1:: 111111 1::111111 1::1111111	Oy 753 IHVISCGYEDKEBMGYGYEDILTGERMHARGWRSYCMPKRARKGSAPINL 812 Db 359 IHVISCGYEDKEBMGKEIGWIYGSVTEDILTGERMHCRAKKSVXVVPRRARKGSAPINL 418 Qy 813 SDRLNQVLRWALGSVEILFSRHCPLWYGYGGRIKFLERPRYTTYPLTSLPLLVVCIL 872 Db 419 SDRLHQVLRWALGSVEILFSRHCPLWYGYGGRIKFLERPRYTTYPLTSLPLLVVCIL 872 Db 419 SDRLHQVLRWALGSVEIFLSRHCPLWYGYGGRIKKWLERLAYINTIVYPFTSIPLLAYCTI 478	QY 873 PAICLITGKFIMPEISNLASIWFIALELSIFATGILEMRWSGVGIDEWWRNEGEWVIGGI 932 11:11 11 1:1:1:1 1 1 1 1 1 1 1 1 1 1 1	Qy 993 VVAGTSYAINSGYOSWGPLFGKLFFAFWIVHLYPFLKGLMGRONRTPTIVIVWAVLLAS 1052	RESULT 11 D86157 Hypothetical protein F22D16.26 - Arabidopsis thaliana hypothetical protein F22D16.26 - Arabidopsis thaliana hypothetical C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana, E.Species: Arabidopsis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.Hin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Rathors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1181 <sto> A; Cross-references: GB:AE005172; NID:g6056428; PIDN:AAF02892.1; GSPDB:GN00141</sto>

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Db 992 TFLIYLLSITLTLCMLSLLEIKWSGITLHEWWRNEQFWVIGGTSAHPAAVLQGLLKVIAG 1051 Qy 950 IDTNFTVTSKAN-DEEGDFAELXWFKWTTLLIPPTTILIINWVGVVAGTSYAINSGYQ 1006 ; : : : : : : : : : : :	QY 539 AGAMNALVRVSAVLTNGQYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRF 598
i ii	QY 659 SLCGGKKRASKSKRKSSDKKKSNRHVDSSVPVFNLEDIEEGVEGAGFDDEKSVLMSQMSL 718
C; Accession: T05646 R; Bewan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999 A; Reference number: 215420 A; Accession: T05646	759 GYEDKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNO
A:Molecule type: DNA A:Residues: 1-1111 <bev> A:Cross-references: EMBL:AL035538 A:Experimental source: cultivar Columbia; BAC clone F20D10 C:Genetics: A:Wap position: 4 A:Introns: 139/2; 675/3</bev>	OY 819 VLAWALGSVEILESRHCPLWYGYGGRLKFLERFATINTTIYPLTSLPLLVYCILPAICLL 878
A, Note: F20D10.310 Query Match 39.1%; Score 2257; DB 2; Length 1111; Best Local Similarity 41.8%; Pred. No. 5.5e-157; Matches 486; Conservative 159; Mismatches 273; Indels 244; Gaps 32;	OY 939 VFOGLLKVLAGIDINFTVTSKANDEEGDFAELXMFKWTTLLIPPTTILIINMVGVVAG 996
3DVCQICADGLGTTLDGDVFTACDVCRFPVCRPCXEHER 54 : : : : :	1026
QY 55 KEGTQACLQCKTKYKRHRGSPAIRGEEGDDTDADDGSDFNYPASGTEDQKQKIADRMRSW 114	OY 1057 LWVRVDPFTTRLAGPNIQTCGI 1078 DD 1086 LWTAINPNTGPAAABGV 1103
QY 115 RMNTGGSGNVGHPKYDSGEIGLSKYDSGEIPRGYVPSVTNSQMSGEIPGASPDHHMMSPT 174	RESULT 13 T51546 cellulose synthase catalytic subunit-like protein - Arabidopsis thaliana
QY 175 GNISRRAPFPYVNHSPNPSREFSGSIGNVAWKERVDGWKMKQDKGAIPMTNGTSIAPSEG 234	ress) g-2000 #text_change 18-Aug-2000
QY 235 RAATDIDASTEYNMEDALLNDETRQPLSRKVPIASSKINPYRMVIVLRLVVLSIFLHYRL 294	R.Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; submitted to the Protein Sequence Database, August 2000 A.Reference number: 225394 A.Accession: 151546
QY 295 THPVRNAYPLWLLSVICEIWFALSWILDQFPKWFPINRETYLDRLALRYDREGEP 349	i
OY 350 SQLAAVDIEVSTVDPLKEEPIVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFDALAET 409 1	A:Experimental source: cultivar Columbia; BAC clone F2KI3 C:Genetics: A:Map position: 5 A:Introns: 297/2; 566/3
Qy 410 SEFARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINA 469 : : ::	38.4%; Score 2220.5; DB 2; Length 1145; 42.4%; Pred. No. 2.8e-154;
OY 470 LVS	MACCHES 4/9; CONSELVATIVE 100; MISMACCHES 280; INGELS 200; CAPS 16 GDVCQICADGLGTTLDGDVFTACDVCRFPVCRPCYEHERKEGTQACLQCKTKYRHRG 73
QY 497DHPGMIQVFLGHSGGLDTEGNELPRLYVSREKRPGFQHHKK 538	DD 125 GSSCAIPGCDAKVMSDERGÖDLLPCE-CDFKICRDCFIDAVKTGGGICPGCKEPYK 179 QY 74 SPAIRGEEGDDTDADDGSDFNYPASGTEDQKQKIADRMRSWRMNTGGSGNVGHPKYDSGE 133

203	SPNP 192	EYNMED 250 MGMEA 271	LSVI 310 : : MSVV 331	FVSTVDPL 365 	КУDI 425 : КНАІ 451	472 HARE 511	VFL- 506 VMLK 570	LTNG 555 :: MSNG 630	IVEF 615 IVEF 689	KRSS 675 : KK 742	-TLM 734 : IPVA 783	MIYG 775 WIYG 843	SRHC 835 : SRNN 903	SIWF 895 :: LVYL 961	: : ISFT 1021	PLFG 1013 	
ENGQQRPMLPGGGGS	SGEIPGASPDHHMMSPTGNIS-RRAPFPYVNH:	AIPMTNGTSIAPSEGRAATDIDAST 	ALLNDETROPLSRKVPIASSKINPYRWVIVLRLVVLSIFLHYRLTNPVRNAYPLWLLSVI 	CEIWFALSWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDF! : :	KEPPIVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFDALAETSEFARKWVPFVKKYDI 	EPRAPEFYECQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVS		GHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNG 	QYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFF ::	DINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKKPGFLASLCGGKKKASKSKKRS : : : : : : DVNMRALDGLMGPVYVGTGCLFRRIALYGFNPPRSKDFSPSCWSCCFPRSKKK-	DKKKSNKHVDSSVPVENLEDIEEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFVAS-TLM	EXGGVPQSSTP	SVTEDILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILF :: ::	PLWYGYGGRLKFLERFAYINTTIYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWF 	IALFLSIFATGILEMRWSGVGIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTNFT	VTSKANDEEGDFAELXMFKWTTLLIPPTTILIINMVGVVAGTSYAINSGYQSWGPLFG 	KLFFAFWVIVHLYPFLKGLMGRQNRTPTIVIVWAVLLASIFSLLWVRVDP 1063 :11:111:
NTHLTDQVD	IGLSKYDSGEIPRGYVPSVTNSQMSGEI	SREFSGS IGNVAWKERVDGWKMKODKG ETTGTYGYGNAFWTKDGDFGSGKDGDG	ALLNDETRQPLSRKVPIASSKINPY : : : : : QDLMSRPWRPLTRKLKIPAGVISPY	CEIWFALSWILDQFPKWFPINRETY : :	KEPPIVTANTVLSILAVDYPVDKVS 	EPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVS- 	KALKVPEF : : : : EIKAMKMQRQNRDDEPMEPVKIPKZ	GHSGGLDTEGNELE	QYMLNLDCDHYINNSKAVREAMCFI::	DINLRGLDGIQGPVYVGTGCVFNR1 : : DVNMRALDGLMGPVYVGTGCLFRR1	DKKKSNKHVDSSVPVFNLEDIEEGV	EYGGVPQSSTP	SVTEDILTGFKMHARGWRSVYCMPK :: :: : SVTEDVVTGYRMHNRGWKSVYCVTR	PLWYGYGGRLKFLERFAYINTTIYE :: : : ALLASSKMKILQRIAYLNYGIYE	IALFLSIFATGILEMRWSGVGIDEW : : :: : :: LIISITLCLLALLEIKWSGISLEEW	VTSKANDEEGDFAELYMFKWTTI: : : LTSKSGGDDIDDEFADLYWVKWTSI	KLEFAFWVIVHLYPFLKGLMGRQNF :1 : : : GVFSFWVLAHLYPFAKGLMGRRGF
180	134	193 236	251 272	311	366	426	473 512	507 571	556 631	616	676	735	776	836	896 962	956 1022	1014
qq	Oy Db	Qy	Qy	Qy Db	Oy Dp	oy Db	Qy Dp	QY	Qy Dp	Qy	Oy Op	6 67 6	Qy Db	Qy	9. Q	Oy Db	Qy Db

Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Issen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter omosome 2 of the plant Arabidopsis thaliana. 3487; PMID:10617197 92924781; PIDN:AAC04910.1; GSPDB:GN00139 -ear cress) 02-Feb-2001 #text_change 02-Feb-2001 VDPLKEPPIVTANTVLSILAVDYPVDKVSCVVS 394 AS-TLMEYGGVP-----0SSTPESLL--- 749 LSKYDSGEIPRGYVPSVTNSQMSGEIPGASPDH 168 ESKGKYGIGNAFWSEEDDTYDGGVSKSD---- 159 ---FLDKPWKPLTRKVQIPAKILSPYRLLIVIR 189 ICEIWFALSWILDQFPKWFPINRETYLDRLALR 342 YDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRR 454 NMREELKEKRIAREKNGGVLPPDGVEVVKATW- 425 RNTVFFDINLRGLDGIQGPVYVGTGCVFNRTAI 642 SKKRSSDKKKSNKHVDSSVPVFNLEDIEEGVEG 702 SGONDYINYTVLMPPTPDNQPAGSSGSTSESKG EFSG - - SIGNVAWKER - - - VDGWKMKQDKGAIP DALLNDETROPLSRKVPIASSKINPYRMVIVLR OVF-----PRG--HSGGLDTEGNEL--PRL AVLTINGOYMLNLDCDHYINNSKAVREAMCFLMD HVRTQSQASQTSQA-----SDLESDTQP TS-----VMKSNNKSMT------ Arabidopsis thaliana re 2212.5; DB 2; d. No. 9.2e-154; Mismatches 266; C:Species: Arabidopsis thallana C:Date: 02-Feb-2001 #sequence_re C:Date: 02-Feb-2001 #sequence_re C:Date: 02-Feb-2001 R:Lin, X.; Kaul, S.; Rounsley, S M.; Koo, H.; Moffat, K.S.; Cront euss, D.; Nierman, W.C.; White, Nature 402, 761-768, 1999 A;Title: Sequence and analysis o A;Reference number: A84420; MUID A;Accession: D84741 A;Rolecule type: DNA A;Rolecule type: DNA A;Rolecule type: DNA A;Rolecule type: DNA A;Gonetics: 1-1036 <270> A;Genetics: At293100 A;Map position: 2 67 KYKRHRGSPAIRGEEGDDTDAD 109 DRMRSWRMNTGGSGNVGHPKYD 283 LVVLSIFLHYRLTNPVRNAYPL DDGASMLTFDALAETSEFARKW 367 WIKREYDEFKVRINGLPEQIKK probable cellulose synthase [imp Query Match 38.3%; Best Local Similarity 43.5%; Matches 481; Conservative 1 84 D-----ANRGGGGGDGPKMGN 169 HMMSPTGNIS-RRAPFPYVNHS 223 MTNGTSIAPSEGRAATDIDAST 484 MQDGTPWPG-----NNTRD 703 AGFDDEKSVLMSQMSLEKRFGQ ||:: || :||| :| | 190 LVIVFFFLWWRITNPNEDAMWL ---SQLAAVD :|: :| | | | | 247 HDKFEQPSPSNPTGRSDLPGVD 307 DDGGAILTFEAMAEAVRFAEYW 455 AMKREYEEFKIRINALVSKALK 426 MADGTHWPGTWFEPKPDHSKGD 523 VYVSREKRPGFQHHKKAGAMNA 583 PNLGPQVCYVQFPQRFDGIDRN 546 RG-GDRICYIQFPORFEGIDPS 643 YGYEPPIKAKKPGFLASLCGGK 117 -LRSQTGDFDHNRWLF----160 -----343 YDREGEP----395 ŏ a q δ q g Db g Ω ò Ω g δ οχ δy 셤 οy g δ g δý q δý ŏ

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C'Accession: C86446
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, M.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Athors: Hunter, J.L.; Y.; Lin, X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Athors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C86446
A;Accession: C86446
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A;Residues: 1-979 <STO>
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A;Cross-references: GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:GN00141
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                                  -----KEAIHVISCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSVYCMPKRP
                                                                                                    AFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTIYPLT
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llarity 44.3%; Pred. No. 3.3e-150;
Conservative 173; Mismatches 245;
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GenCore version 5.1.3
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OM protein - protein search, using sw model

February 19, 2003, 16:34:11 ; Search time 34 Seconds (without alignments) 1317,483 Million cell updates/sec Run on:

US-09-900-237-30 5778 1 MDGDADALKSGRHGAGDVCQ......VDPFTTRLAGFNIQTCGINC 1080 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	, Q	093in2 salmonella	Q59167 acetobacter	Q8x517 escherichia	_	P58931 pseudomonas		Q9rbj2 acetobacter	Q9wx75 acetobacter			P21877 acetobacter							Q64398 mesocricetu	mus	-		schizos		P78953 schizosacch	P77933 pyrococcus	P26660 h genome po	7.0	canis far	543	307 caenorhal	5575	P20681 podospora a
SUMMARIES	ID	BCSA SALTI	BCSA_SALTY	ACS2_ACEXY	BCSA_ECO57	BCSA_ECOLI	BCSA_PSEFL	BCA1_ACEXY	BCA4_ACEXY	BCA5_ACEXY	BCA2_ACEXY	BCSA_XANAC	ACS1_ACEXY	BCA3_ACEXY	SUBF_BACSU	YCDQ_ECOLI	NUIM_STRPU	RIP3_RAT	YOAB_BACSU	KDGD_MESAU	RIP3_MOUSE	TPP2_MOUSE	CLAA_BACTU	ME21_SCHPO	ICPO_HSV11	DMF1_SCHPO	DPOL_PYRKO	POLG_HCVJ6	TPP2_RAT	G6PT_CANFA	CYOB_BUCAI	YKR1_CAEEL	- 1	COX1_PODAN
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ALIGNMENTS

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AICLLTGKFIMPEISNLASIWFIALFLSIFA-TG 906	RT; 874 AA. ence update) tation update) bunit [UDP-forming] (EC 2.4.1.12). subdivision; Enterobacteriaceae;	okranz W., Roemling U.; okranz W., Roemling U.; of Salmonella typhimurium and ose as the second component of the 01). 33; Berasain C., Ghigo JM., Gamazo C., enteritidis biofilm formation:	O720; Spieth J., Clifton S.W., Latrellle P., J., Dante M., Du F., Hou S., Layman D., J., Holmes A., Grewal N., Mulvaney E., ler W., Stoneking T., Nhan M., lmonella enterica serovar Typhimurium of cellulose synthase. It polymerizes cose to cellulose, which is produced as for mechanical and chemical protection ary phase, when the cells exhibit r morphotype). Co-expression of ive fimbriae leads to a hydrophobic cells embedded in a highly inert cose + {(1,4-beta-D-glucosyl})(N) = UDP Hilarity). dby bis-(3'-5') cyclic diguanylic acid
848 LERFAYINTTIYPLTSLPLLVY 1 1 1 1 1 1 1 1 1 1	3 1 -	HU / PEG 1	SEQUENCE FROM N.A. STRAIN=LT2 / SGSC1412 / AT MEDLINE-21534948: PubMed=1 MCDLelland M., Sanderson K Courtney L., Porwollik S., Leonard S., Nguyen C., Sco Ryan E., Sun H., Florea L. Waterston R., Wilson R.K.; "Complete genome sequence LT2."; Nature 413:852-856(2001)! FUNCTION: Catalytic su uridine 5' diphosphate an extracellular compa at the onset of the st multicellular behavior cellulose and thin agg network with tightly F matrix. + (1.4-beta-D-glucosy -! COFACTOR: Magnesium (H -! COFACTOR: Magnesium (H -! ENZYME REGULATION: Act (C-di-GMP) (By similar
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                                     DOMAIN: There are two conserved domains in the globular part of the protein: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the QXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain
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PATHWAY: Bacterial cellulose biosynthesis.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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SUBSTRATE BINDING (POTENTIAL).
1; 4C9421B58606310A CRC64;
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InterPro; IPR005150; Cellulose_synt.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00525; Cellulose_synt; 1.
Pfam; PF00535; Glycos_transf_2.1.
Cellulose biosynthesis; Transferase;
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-!- DOMAIN: There are two conserved domains in the globular part of the catalytic subunit: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the QXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain in the active site.
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J. Bacteriol. 177:5276-5283(1995).
-!- CATALYTIC ACTIVITY: UDP-glucose + {(1,4-beta-D-glucosyl})(N) = UDP + {(1,4-beta-D-glucosyl)}(NN11).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cellulose synthase 2 [Includes: Cellulose synthase catalytic subunit
[UDP-forming] (EC 2.4.1.12); Cyclic di-GMP binding domain (Cellulose synthase 2 regulatory domain)].
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  GQYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRF---DGIDRN----DRY
                                                                                           608 ANRNTVFFDINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKKPGFLASLCGGKKKA
                                                                                                                         353 GEFVAIFDCDHVPTRSFLQMTMGWFLKE----KQLAMMOTPHHFFSPDPFERNLGRFRKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Profeobacteria; alpha subdivision; Acetobacteraceae;
Gluconacetobacter.
NCBI_TaxID=28448;
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MEDLINE=95394846; PubMed=7665515;
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Qγ	ΩD	Qy	qa	QY	ΩD	Qy	qα	QY	qa	0λ	Dp	Qy	QQ	RESULT	BCS ID	AC DT	TQ TQ	DE	80 00 00	8 8 8 8 8	RN	R R	RA RA	RA RA RA	F 7	X X t	Z X Z	RA E	R R R	RE	888	388	388
this strain.	-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.	C -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ACSB/BCSB	This SWISS-PROT entry is copyright. It is produced through	Delween the Swiss institute of bioinformatics and the Ernbi Outstated the European Bloinformatics Institute. There are no restrictions on the European Bloinformatics institute.	use by non-proist institutions as lor modified and this statement is not remov					Production Products Product		Transmembrane; Inner membrane. DOMAIN 1 749 CATALYTIC.	750 1596 145 238 315 375	TRANSMEM 25 45 TRANSMEM 106 126	TRANSMEM 396 416 TRANSMEM 421 441	TRANSMEM 505 TRANSMEM 544	TRANSMEM 1553 1573 ACT_SITE 187 187	ACT_SITE 331 331 POTENTIAL. SITE 234 234 SITE BINDING	SITE 236 236 SUBSTRATE STORE 1596 AA: 175799 MW. D9RAFE	Query Match 4.5%; Score 259.5; DB 1;	est Local Similarity 18.0%; Pred. No. 6.1e-10; atches 144; Conservative 101; Mismatches 212; Indels 34	Qy 278 VIVLRLVVLSIFLHYRLTNPVRNAYPLWLLSVICEIWFALSWILDQF 324	::: : ::	QY 325 PKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPLKEPPIVTANTVLSILAVDY 384		Db 176 PADKLNVYILDDG188	QY 445 VQPSFVKDRRAMKREYEEFKIRINALVSKALKVPEEGWIMQDGTPWPGNNTRDHPGMIQV 504	Db 189211	QY 505 FLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCD 564	TOTAL DESCRIPTION OF THE PROPERTY OF THE PROPE	UY 505 HIINBSKAVKRAMCELEMURNASPYOVCYVQEPOKFDELDKNDKYANKNIVTEDI 01/ DD 237 H-IPTRGFLKKTIGWMMADPKLALLQTPHHFYSPDFFQRNLATGONVPPEGNMFYGL 292	Qy 618 NLRGLDGIQGPVYVGTGCVENRTALYGYEPPIKAKKPGFLASLCGGKKKASKSKKRSSDK 677	Db 293 VQDGNDFWDATFFCGSCAAIRRSAVLGI320
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	YPEISNLASIW-FIALFLSIFATGILEMRWSGVG 916 :	0.4.0	700927; 51; rland V., Mau B., Glasner J.D., .S., Gregor J., Kirkpatrick H.A., .Boutin A., Shoo Y., Miller L., A., Dimalanta E.T., Potamousis K., Lin J., Yen G., Schwartz D.C., rrhagic Escherichia coli 0157:H7.";	M., Kurokawa K., Ishli K., Yokoyama K., K., Murata T., Tanaka M., Tobe T., Sakawa C., Ogasawara N., Yasunaga T., Shinagawa H., terohemorrhagic Escherichia coli with a laboratory strain K-12."; of cellulose synthase. It polymerizes ose to cellulose, which is produced as for mechanical and chemical protection ary phase, when the cells exhibit x morphotype). Co-expression of live fimbriae leads to a hydrophobic cells embedded in a highly inert
678 KKSNKHVDSSVPVFNLEDIEEG 321	858 IYPLTSLPLLVYCILPAICLIT 403 SHFLFAIPRLVFLASPLAFLFL 917 IDEWWRNEOFW-VIGGISAHLE 459RYSFWSEIYETTIALE 976 TTLLIPPTILIINWCVVAG- : : : : 508 -NAVYPNVILAVILALALVRGI 1022 IVHLYPFLKGL-WGRQNR 103	JLT 4 BCSA_ECO57 BCSA_ECO57 STANDARD; QRX517; 15-070-2002 (Rel. 41, Last 15-370-2002 (Rel. 41, Last 15-370-200 (Rel. 41), Last 15-370-200 (Rel. 41), Last 15-370-200 (Rel. 41) 15-370-200 (Rel. 41) 16-370-300 (Rel. 41)	STRAIN-0157-H7 / EDL933 / MEDLINE-21074955; PubMed-11 Perna N.T., Plunkett G. II Rose D.J., Mayhew G.F., Evr Posfai G., Hackett J., Kli Grotbeck E.J., Davis N.W., Apodaca J., Anantharaman T. Welch R.A., Blattner F.R.; "Genome sequence of entero Nature 409:529-533(2001).	SECOLOCIE FOR NO. N. S.
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                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                       DOMAIN: There are two conserved domains in the globular part of the protein: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the OXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain the active site.
CATALYTIC ACTIVITY: UDP-glucose + {(1,4-beta-D-glucosyl)}(N) = UDP
                                  cyclic diguanylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKVPIASSKINPYRMVIVLRLVVLSIFLHYRLT-----NPVRNAYPLWLLSVICEIWFA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMPGRESAL----MLIVLSLIVSCRYIWWRYTSTLNWDDPVSLVCGLILLFAETYAWIV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFVSTVDPLKEPPIVTANTV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L--VLGYFQVVWPLNRQP----VPLPKDMSLWPS----VDIFVPTYN---EDLNVVKNTI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQ 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VKYIARTT----HEHAKAGNINNALKYA----KGE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212; Indels 374;
                                                                                                                                                                                   SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 872;
                                                     PATHWAY: Bacterial cellulose biosynthesis.
SUBCELLULAR LOCATION: Integral membrane protein. Inner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBSTRATE BINDING (POTENTIAL)
SUBSTRATE BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                       Cellulose biosynthesis; Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. ATALYTIC SUBDOMAIN ATALYTIC SUBDOMAIN
         + {(1,4-beta-D-glucosyl)}(N+1).
COFACTOR: Magnesium (By similarity).
ENZYME REGULATION: Activated by bis-(3'-5')
(c-dl-GMP) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F3F1A24A2B713FBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 258; DB 1;
Pred. No. 3.1e-10;
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                                                                                                                                                                                                                                                                                                      EMBL; AP005579; AAG58675.1; ALT_INIT.
EMBL, AP002565; BAR31836.1; ALT_INIT.
LINEMPRO; IPRO0173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                                                                                                                                                                                                                                   Inner membrane;
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872 AA;
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                                                                                 (Potential).
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970 LYMFKWTTLLIPPTTILIINMVGVVAGTSYAINSGYQSWGPLFGKL
                                                                                                 FYSIFDCDHVPTRSFLQMTVGWFLKE----KQLAMMQTPHHFFSPDPFERNLGRFRKTPN 410
YMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRF---DGIDRN----DRYAN 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---LDEIGGI-----TVTEDAHTSLRLHR 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGYTSAYM -- RIPQAAGLATESLSAHIGQRIRWARGMVQI-FRLDNPL---TGKGLKFAQ 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RFAYINTTIYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFLSIFATGILE 909
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKKRSSDKKKSNKHVDSSVPVFNLEDIEEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFV
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                                                                                                                                                                                                                                                         RNTVFFDINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKKPGFLASLCGGKKKASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          730 ASTLMEYGGVPQSSTPESLLKEAIHVISCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHA
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Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                             411 EGTLFYGLVODGNDMWDATFFCGSCAVIRR--------KP-----
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CHARACTERIZATION.
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PubMed=11260463;
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: There are two conserved domains in the globular part of the protein: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the OXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain in the active site.
                                                                                                                                                                                                                                                                        + {(1,4-beta-D-glucosyl)}(N+1).
COFACTOR: Magnesium (By similarity).
ENZYME REGULATION: Activated by bis-(3'-5') cyclic diguanylic acid
                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: UDP-glucose + {(1,4-beta-D-glucosyl})(N) = UDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: The genes bscA, bcsB, bcsZ and bcsC are constitutively transcribed but cellulose synthesis occurs only when adrA, a putative transmembrane protein regulated by agfD, is expressed. Cellulose production is abolished in E.coli K12. SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. CAUTION: Ref. 1 sequence differs from that shown due to a frameshift in position 128.
                                                                                          PRICEORY Catalytic subbnit of cellulose synthase. It polymerizes uridine 5'-diphosphate glucose to cellulose, which is produced as an extracellular component for mechanical and chemical protection at the onset of the stationary phase, when the cells exhibit multicellular behavior (rdar morphotype). Co-expression of cellulose and thin aggregative fimbriae leads to a hydrophobic
                                                                                                                                                                                                                                                                                                                                  (c-di-GMP).
PATHWAY: Bacterial cellulose biosynthesis.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
Zogaj X., Nimtz M., Rohde M., Bokranz W., Roemling U.;
"The multicellular morphotypes of Salmonella typhimurium and
Escherichia coli produce cellulose as the second component of the
                                                                                                                                                                                                                network with tightly packed cells embedded in a highly inert
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SUBSTRATE BINDING (POTENTIAL).
14326B8A2EB228F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF00535; Glycos_transf_2; 1.—
Cellulose biosynthesis; Transferase; Glycosyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U00039; AAB18511.1; ALT_FRAME.
EMBL; AE000430; AAC76558.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U00039; AAB18510.1; ALT_FRAME.
                                                                              Mol. Microbiol. 39:1452-1463(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99784 MW;
                                                              extracellular matrix.";
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872 AA;
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                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
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Length 872;

Score 257; DB 1; Pred. No. 3.7e-10;

4.48;

Query Match Best Local Similarity

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ISYAINSGYOSWGPLFGKL------FFA 1018
                                                                                                                                                                                                                                                                                                            --KOLAMMOTPHHFFSPDPFERNLGRFRKTPN 410
                                                                                                                                                                                                                                                                                                                                                               IRR----- 442
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                                                                                          DALAETSEFARKWVPFVKKYDIEPRAPEFYFCQ 436
                                                                                                                                                                                                                                                                                     NLGPQVCYVQFPQRF---DGIDRN----DRYAN 609
                                                                                                                                                                                                                                                                                                                                       FNRTALYGYEPPIKAKKPGFLASLCGGKKKASK 669
                                                                                                                                                                                                                                                                                                                                                                                         EEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFV 729
                                                                                                                                                                                                                                                                                                                                                                                                                                         SCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHA 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IHASL-TNSKIQGKY--RHSFWSE 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PHKGKFNVTAKGGLVEEEYV 631
                         LHYRLT-----NPVRNAYPLWLLSVICEIWFA 316
                                                   IWWRYTSTLNWDDPVSLVCGLILLFAETYAWIV 246
                                                                             DREGEPSQLAAVDIFVSTVDPLKEPPIVTANTV 376
                                                                                                                                                                                 KIRINALVSKALKVPEEGWIMQDGTPWPGNNTR 496
                                                                                                                                                                                                                                                            IARTT----KGE 354
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unit [UDP-forming] (EC 2.4.1.12).
Mismatches 212; Indels 374;
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P58931;
15-JUN-2002 (Rel. 41, Creat
15-JUN-2002 (Rel. 41, Last
15-JUN-2002 (Rel. 41, Last
                            RKVPIASSKINPYRMVIVLRLV
                                         DHPGMIQVFLGHSGGLDTEGNE
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                                                                              LSWILDQFPKWFPINRETYLDR
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L--VLGYFQVVWPLNRQP---
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NCBI_TaxID=294;
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PubMed=11297407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                         (Potential).

DOMAIN: There are two conserved domains in the globular part of the protein: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the QXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain in the active site.
                                                                   + {(1,4-beta-D-glucosyl)}(N+1).
COFACIOR: Magnesium (By similarity).
ENZYME REGULATION: Activated by bis-(3'-5') cyclic diguanylic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spiers A.J., Kahn S.G., Bohannon J., Travisano M., Rainey P.B.; "Adaptive divergence in experimental populations of Pseudomonas fluorescens. I. Genetic and phenotypic bases of wrinkly spreader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85; Mismatches 212; Indels 348;
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SUBSTRATE BINDING (POTENTIAL).
SUBSTRATE BINDING (POTENTIAL).
W; 2B962EA3854B23BB CRC64;
                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2
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Transmembrane; Inner membrane.
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Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 248;
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CATALYTIC :
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                  MEDLINE-22013850; PubMed=12019221;
Spiers A.J., Kahn S.G., Bohannon J.,
"Adaptive divergence in experimental
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739 AA;
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Matches 155; Conserv
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GIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINMVGVVAGTSYAINSGYQSW 1008
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"Genetic organization of the cellulose synthase operon in Acetobacter
                                                                                                                                                                                                                 OMSLEKRFGQSAAFVASTLMEYGGVPQSSTPESLLKEAIHVISCGYEDKSEWGTEIGWIY 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            835 CPLWYGYGGRLKFLERFAYINTTIYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASIW 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 NPL---LGKGLKWGQRICYANAMQHFFYGLPRLVFLTAPLAYLIFG----AEIFHASALM 447
YDIEPRAPEF-YFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVSKALKVPEEG 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSVTEDILIGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRH
                                                                                                                                           WIMODGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGA
                                                                                                                                                                                                                                                                                           MNALVRVSAVLTNGQYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DGIDRN-DRY---ANRNIVFFDINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKKP
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cellulose synthase catalytic subunit [UDP-forming] (EC 2.4.1.12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong H.C., Fear A.L., Calhoon R.D., Eichinger G.H., Mayer R.,
Amikam D., Benziman M., Gelfand D.H., Meade J.H., Emerick A.W.,
Bruner R., Ben-Bassat A., Tal R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
Gluconacetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 25-42 AND 196-206
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MEDLINE=91045951; PubMed=2146681;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
Chang A.L., Tuckerman J.R., Gonzalez G., Mayer R., Weinhouse H., Volman G., Amikam D., Benziman M., Gilles Gonzalez M.-A.;
"Phosphodiesterase Al. a regulator of cellulose synthesis in Acetobacter xylinum, is a heme-based sensor.";
Biochemistry 40:3420-3426(2001).
-! FOWGTION: Catalytic subunit of cellulose synthase. It polymerizes uridine 5'-diphosphate glucose to cellulose in a processive way. The thick cellulosic mats generated by this enzyme probably provide a specialized protective environment to the bacterium.
-! CATALYTIC ACTIVITY: UDP-glucose + {(1,4)-beta-D-glucosyl}(N) - UDP + {(1,4)-beta-D-glucosyl}(N+1).
-! COFACTOR: Magnesium.
-! EXECULATION: Activated by bis-(3'-5') cyclic diguanylic acid
                                                                                                                                                                                                                                                                             Cochectal).

DOMAIN: There are two conserved domains in the globular part of the catalytic subunit: the N-terminal domain (domain A) contains the conserved by motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the CXRW motif and is present only in processive glycosyl transferases. It could be involved in the processive glycosyl the enzyme, possibly required for holding the growing glycan chain in the active site.

INDUCTION: Callulose is produced at a linear rate with respect to cell growth when O(2) is present.

SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 -INRETY-LDRLALRYDREGEPSQLA------AVDIFVSTVDPLKEPPIVTANT 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.1%; Score 238.5; DB 1; Length 754;
20.1%; Pred. No. 6e-09;
tive 82; Mismatches 232; Indels 335; Gaps
                                                                                                                                                                                                                                            PATHWAY: Excterial cellulose biosynthesis.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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SUBSTRATE BINDING (POTENTIAL).
SUBSTRATE BINDING (POTENTIAL).
8D5FC1FE62E2C068 CRC64;
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InterPro: IPR003919; Cellsynth_A.
InterPro: IPR001313; Glycos_transf_2.
Pfam: PR00535; Glycos_transf_2.1.
PRINTS; PR01439; CELLSNTHASEA.
Cellulose biosynthesis; Transferase; Glycosyltransferase;
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CATALYTIC SUBDOMAIN B.
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<pre>genes from Acetobacter xylinum JCM t of cellulose synthase genes.";</pre>	"Cloning of cellulose synt 7664: implication of a nov	RT
iyama H., Onizuka T., Ike	362906; Hirano A., I	ra Ra
	SEQUENCE FROM N.A. STRAIN-JCM 7664 / IFO 1369;	RR
	Gluconacetobacter. NCBI_TaxID=28448;	888
subdivision; Acetobacteraceae;	Acetobacter xylinus. Bacteria; Proteobacteria;	800
gulatory subunit)].	domain (Cellulose synthase BCSABII-A.	E G G
Includes:	Putative cellulose synthas	100
ance	15-JUN-2002 (Rel. 41, Creat 15-JUN-2002 (Rel. 41, Last 15-JUN-2002 (Rel. 41, Last	355
		AC
RI; 1518 AA.	RESULT 8 BCA4_ACEXY ID BCA4_ACEXY STANDARD;	RESUI BCA4_ ID
VLAST 1053 	102/ PFLKGLMGRONRTPT1VIVWA- : : 538NOLAGIAKRAYLLNCIWAM	y g
AGIMTLGLLIGLFELTFHF 537	511 ATYPNIIF	qa
AGTSYAINSGYQSWGPLFGKLFFAFWVIVHLY 1026	969 ELYMFKWTTLLIPPTTILIINK	ΟŊ
:: :: :	452 TAAKVNKGWR-YSFWSEVYETI	Q
AVFQGLLKVLAGIDTNFTVTSKANDEEGDFA 968	914 -GVGIDEWWRNEQFW-VIGGIS	Qy
*IMPEISNLASIWETALE LOIFAIGILLEGAMS	850 TIIYLISLELLVICLLFALCE :: :: 403 AMTSFERIDBVIELASDLAE	ਨੇ ਵੰ
LS 40		qq
MALGSVEILFSRHCPLWYGYGGRLKFLERFAYIN 855	796 YCMPKRPAFKGSAPINLSDRLN	δy
:	314	qq
DKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSV 795	736 YGGVPQSSTPESLLKEALHVIS	Qy
DGND	286	ΩD
SAGEDDEKSVLMSQMSLEKRFGQSAAFVASTLME 735	676 DKKKSNKHVDSSVPVFNLEDIE	QY
AVGYRTP 285	273PF	đ
YGYEPPIKAKKPGFLASLCGGKKKASKSKKRSS 675	616 DINLRGLDGIQGPVYVGTGCVF	δλ
DRKIALMQTPHHFYSPD272	: :: 230 DYILILDCDH-IPTRAFLQIAM	qa
PNLGPQVCXVQEPQRFDGIDRNDRYANRNTVFF 615	556 QYMLNLDCDHYINNSKAVREAN	QY
NLNHAI	206YIGRVDSS	QQ
JVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNG 555	496 RDHPGMIQVFLGHSGGLDTEGN	δŏ
FAKDCGAL 205	: 191VRP	qa
FFKIRINALVSKALKVPEEGWIMQDGTPWPGNNT 495	436 OKIDYLKDKVOPSFVKDRRAMK	Qy
190	: :	qq
FDALAETSEFARKWVFVKKYDIEPRAPEFYFC 435	376 VLSTLAVDYPVDKVSCXVSDDG	ò

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SEQUENCE FROM N.A.
STRAIN-JCM 7664 / IFO 13693;
PubMed=10382968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
----RRKAFHDFAVEAGA-
                                              --AENN-----
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                                                                   DOMAIN: There are two conserved domains in the globular part of the catalytic subunit: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the OXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain the active site.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
           UDP-glucose + {(1,4-beta-D-glucosyl})(N) = UDP
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         CATALYTIC ACTIVITY: UDP-glucose + {(1,4-beta-D-glucosyl})(N) = U + {(1,4-beta-D-glucosyl)}(N+1) = PATHNAY: Bacterial = Cellulose biosynthesis.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315;
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Pred. No. 1.7e-08;
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InterPro; IPR003919; Cellsynth,A.
InterPro; IPR003920; Cellsynth,B.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00235; Glycos_transf_2.
PRINTS; PR01440; CELLSWIHASEB.
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Conservative
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235 23
1518 AA;
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Matches 147; Conserv
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----LIINMVGVV-----AGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGL-M 1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YAPDP-----FORNLAGG-------MHVPPEGNMF 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      692 NLEDIEEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFVASTLMEYGGVPQSSTPESLLKE 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             752 AIHVISCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSVYCMPKRPAFKGSAPIN 811
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative cellulose synthase 3 [Includes: Cellulose synthase
catalytic subunit [UDP-forming] (EC 2.4.1.12); Cyclic di-GMP binding
domain (Cellulose synthase 3 regulatory subunit)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Potential).
-!- DOMAIN: There are two conserved domains in the globular part of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 AVREAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFFDINLRGLDGIQGPVYV
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LDT EGNEL PRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHY INNSK
                                                                                                                                       -----HAKAGNLNHALAV----TDSPFAVIFDCDHVPTRGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCVFNRTAIYGYEPPIKAKKPGFLASLCGGKKKASKSKKRSSDKKKSNKHVDSSVPVF
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Gluconacetobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
the catalytic subunit: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the OXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain in the active site.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.

SIMILARITY: IN THE C-TERMINAL SECTION; DELONGS TO THE ACSB/BCSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 IMMLSLLVSLRYIVWRLTATVQ - · FSNWLQTALAVLLLLAEAYALMTLCLSYFQMAWPLR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 YILDDG ----- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRRAMKREYEEFKIRINALVSKALKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYINNSK 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.1%; Score 238.5; DB 1; Length 1518;
Best Local Similarity 18.7%; Pred. No. 1.7e-08;
Matches 147; Conservative 99; Mismatches 224; Indels 315; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 VIVLRLVVLSIFLHYRLTNPVRNAYPLWL-----LSVICEIWFALSWILDQFPKWFPIN 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RETYLDRLALRYDREGEPSQLAAVDIFVSTVDPLKEPPIVTANTVLSILAVDYPVDKV$C 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 YVSDDGASMLTFDALAETSEFARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC.
CYCLIC DI-GMP BINDING (BY SIMILARITY).
CATALYTIC SUBDOMAIN A.
CATALYTIC SUBDOMAIN B.
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IMPORTANT FOR SUBSTRATE BINDING
                                                                                                                                                                                                                                                                                                                  EMBL; AB015804; BAA77600.1; -.
InterPro; IPR003919; Cellsynth_A.
InterPro; IPR001920; Cellsynth_B.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2.
PRINTS; PR0149; CELLSWTHASEA.
PRINTS; PR01440; CELLSWTHASEA.
Cellulose biosynthesis; Transferase; Glycosyltransferase;
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DGIDRNDRYANRNTVEFDINLRGLDGIQGPVYV 63 SLCGGKKKASKSKKRSSDKKKSNKHVDSSVPVF 69 1	FWDATFEGSCAIIRRE 314 EDILTGEKNHARGWRSVCMPKRPAFKGSAPIN 811	AT; 756 AA. ance update) tation update) bunit (UDP-forming] (EC 2.4.1.12). subdivision; Acetobacteraceae; Tsuchida T., Yoshinaga F., Sakai F., Hayashi T.; ellulose synthase (bcsA) promoter bPR 2001."; of cellulose synthase. It polymerizes ose to cellulose. The thick cellulosic me probably provide a specialized he bacterium (By similarity). cose + f(1.4)-beta-D-glucosyl)(N) - UDE +1). d by bis-(3'-5') cyclic diguanylic acid b by bis-(3'-5') cyclic diguanylic acid cost membrane protein. Inner membrane rved domains in the globular part of
AVREAMCFLMDPNLGPQVV	289YGLVQDGND 752 AIHVISCGYEDKSEWGTEIGWI 315 AVMGIG	BCA2_ACEXY ID BCA2_ACEXY TO BCA2_ACEXY TO G82859; DT 15-JUN-2002 (Rel. 41, Creat) DT 15-JUN-2002 (Rel. 41, Last) DE Cellulose synthase catalyt. GN BCSA. S Acetobacter xylinus. GN BCCAN. S Acetobacter xylinus. C Bacteria; Proteobacteria; Proteobacteri
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the catalytic subunit: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the QXXRM motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of
                                                                                                                            the enzyme, possibly required for holding the growing glycan chain in the active site. SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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SUBSTRATE BINDING (POTENTIAL).
SUBSTRATE BINDING (POTENTIAL).
W; 6954F39A25E73B0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulose biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC SUBDOMAIN B CATALYTIC SUBDOMAIN B POTENTIAL. POTENTIAL.
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InterPro; IPR003919; Cellsynth_A.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; PRINTS; PR01439; CELLSNTHASEA.
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756 AA;
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A Silva A.C.R., Ferrod.J.A., Relach F.C., Farah C.S., Furlan L.R., R.A. Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., Almeida N.F., Camarotte G., Cannavan F., Cardazo J., Chambergo F., Ciapina L.P., R. Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Ratia J.B., Ferrelara A.G., Ferro M.I.T., Ratia J.B., Ferrelara R.C., Greegio C.C., Ferro M.I.T., Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Lorali B.C., Machado M.A., Madeira A.M., M., Mattinez-Rossi N.M., Martins E.C., Machado M.J., Moro K.C.F.M., Myaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Prindade dos Santos M., Tuffil D., Silva C., de Souza R.F., Spinola L.A.F., Taxita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Shon J.J., Milte F.F., Comparison of the genomes of two Xanthomonas pathogens with differing R.T. host specificities.";

Nature 417:459-463(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- CATALYTIC ACTIVITY: UDP-glucose + {(1,4-beta-D-glucosyl})(N) = UDP + {(1,4-beta-D-glucosyl)}(N+1).
-:- COFACTOR: Magnesium (By similarity).
-:- ENZYME REGULATION: Activated by bis-(3'-5') cyclic diguanylic acid (c-di-GMP) (By similarity).
-:- PATHWAY: Bacterial cellulose biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Catalytic subunit of cellulose synthase. It polymerizes uridine 5'-diphosphate glucose to cellulose, which is produced as an extracellular component for mechanical and chemical protection
                                                                                                                                                                                                                                                                                                 425 FLFAGONII------AAAPLAVAAYALPHMFHSIATAAKVNKGWR-YSFWSEVYE 472
IEEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFVASTLMEYGGVPQSSTPESLLKEAIHV 755
                                                                                                                                  IG------GFAVETVTEDAHTALRMQRRGWSTAYL--RIPVASGLATERLTTH 368
                                                                                                                                                                                                          876 CLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWS----GVGIDEWWRNEQFW-VIGG 931
                                                                                                                                                                                                                                                                                                                                                             932 ISAHLFAVFQGLLKVLAGIDTNFTVTSKA---NDEEGDFAELY-MFKWTTLLIPPTTI-- 985
                                                                                                                                                                                                                                                                                                                                                                                                      473 TIMALFLVRVIIVILLFPSKGKFNVTEKGGVLEEEEFDLGATYPNIIFATIMMGGLLIGL 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                      --LII--NWGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGL-MGRQNR 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | : | : | : | : | : | : | 533 FELIVRENOLDVIARNAYLLNCA------WALISLIILFAAIAVGRETK 575
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                                                                                         ISCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDR
                                                                                                                                                                                LNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTTIYPLTSLPLLVYCILPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2003 (Rel. 41, Last annotation update)
Cellulose synthase catalytic subunit [UDP-forming] (BC 2.4.1.12).
BCSA OR XAC3518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity)
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BCSA_XANAC
ID BCSA_XANAC
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the protein: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the CXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain in the active site.	sierase; Glycosyltransferase; CATALYTIC SUBDOMAIN A. CATALYTIC SUBDOMAIN B. POTENTIAL.	tch al Similarity 19.2%; Pred. No. 2.3e-08; 149; Conservative 94; Mismatches 211; Indels 324; Gaps 31; VIVLRIVVLSIFLHYRLTNPVRNAYPLWLLSVICEINFALSWILDQFPRWF 328 :: : VYILMMMGNSLAVSCRYIWNRMTQTMGVGSAVDFILGLGLEGAELYAFVILVLGYFQVLW 136	PINRETYLDRIALRYDREGEPSQLAAVDIEVSTVDPLKEPPIVTANIYLSILAVDYPVDK 388 : :	SFVKDRRAMKREYEEFKIRINALVSKALKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLG 507	HSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLINGQYMLNLDCDHYI 567 	NNSKAVREAM-CFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFFDINL 619 ::	RGLDGIQGPVYVGFGCVFNNTAIYGYEPPIKAKKPGFLASLCGGKKKASKSKKRSSDKKK 679 	SNKHVDSSVPVFNLEDIEEGVEGAGFDDEKSVIMSQMSLEKRFGQSAAFVASTLMEYGGV 739	740 POSSTPESLLKEALHVISCGYEDKSEWGTEIGWIYGSVTEDILIFGFKMHARGWRSVYCMP 799
the protein: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catal substrate binding. The C-terminal domain (domain B) conta CAXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity in the enzyme, possibly required for holding the growing gly in the active site.	Cellulose blosynthesis; Transferase; Transmembrane; Inner membrane. Transmem 30 50 POTENTI TRANSMEM 110 130 POTENTI TRANSMEM 405 447 POTENTI TRANSMEM 427 447 POTENTI TRANSMEM 427 447 POTENTI TRANSMEM 520 540 POTENTI TRANSMEM 540 569 POTENTI TRANSMEM 540 560 POTENTI STITE 240 SUBSTRANSMEM 540 SUBSTRANSMEM	Query Match Best Local Similarity 19.2%; Pr Matches 149; Conservative 94; 278 VIVLRLVVLSIFLHYRLTNP- 1:: :: :: :: : : : : : : : : :	329 PINRETYLDRIALRYDREGEPSGLAP 137 PLNRKPVPLPADGRLWPS 389 VSCYVSDDGASMLTFDALAETSEFAB :: : 186 ITIHLLDDG	448 SFVKDRRAMKREYEEFKIRINALVSK	508 HSGGLDTEGNELPRLYYVSREKRPGF :: : 207GINYVTRTNNA	568 NNSKAVREAM-CFLMDPNLGPQVCYVQFPQRFDGIDRN 1 :	620 RGLDGIQGPVYVGTGCVFNRTAIYGY 	680 SNKHVDSSVPVFNLEDIEEGVEGAGF	740 PQSSTPESLLKEAIHVISCGYEDKSE
888888888888888888	OCC KWW KWW KWW KWW KWW KWW KWW FT	A WE DO	6 6 6	oy D	Oy Op	Oy Dp	oy D	Oy Dp	ογ

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SALMILAYALPHILQANLTNIRVQSRFRHLLWN 470
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an operon for cellulose biosynthesis
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-----TVTEDAHTALKLQRRGYRTAYLAV 356
                                                                                                                                                                   SNLASIWFIALFLSIFATGI-LEMRWSGVGID 918
                                                                                                                                                                                                                                                               VLAGIDT-NFTVTSKA----NDEEGDFAELYM 972
                                                                                                                                                                                                                                                                                                               ALLNPKLGKFNVTPKGGLVARSYFDAQIAKPYL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cation update)
Cellulose synthase catalytic domain
Lic di-GMP binding domain (Cellulose
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ne cellulose-synthesizing operon (acs
implications for cellulose
                                                                                                                                                                                                                                                                                                                                                                SYAINSGYOS -- WGPLFGKLFFAFWVIVHL 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \hat{\mathbf{d}}, \mathbf{Jr.}; pellulose synthase catalytic subunit
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                                                                                                   VEILFSRHCPLWYGYGGRLKFLERFAYINTTIY
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STRAIN-ATCC 5582,
MEDLINE-91346705; PubMed-2:
Saxena I.W., Lin F.C., Bro-
"Cloning and sequencing of
gene of Acetobacter xylinu
Plant Mol. Biol. 15:673-68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACSI_ACEXY STANDARD;
P21877;
P
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STRAIN-AFTCC 53582;
MEDLINE-91322609; PubMed-16
Saxena I.M., Lin F.C., Broy
"Identification of a new 9
in Acetobacter xylinum.";
Plant Mol. Biol. 16:947-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Faxer John, Kudlicka K.,
"Characterization of genes
openon) of Acetobacter xyl
crystallization.";
J. Bacteriol. 176:5735-575
                                                                    800 KRPAFKGSAPINLSDRLNQVLR
| | | | :| :| :|
357 --PQAAGLATESLSGHVAQRIR
                                                                                                                                                                                                                                                                                                                                                                                         | :|:|:||F------ELLLINVGMV
                                                                                                                                                                     860 PLTSLPLLVYCILPAICLLTGR
                                                                                                                                                                                                                   411 FFYGVPRIIYLTAPLAYLFFG
                                                                                                                                                                                                                                                                    EWWRNEQFWVIGGISAHLFAVE
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STRAIN-ATCC 23769;
MEDLINE-94131945; Pubmed-8
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                                                                                                                                                                                                                                                                                                               EVYETTLAWYI -----
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Bacteria; Proteobacteria;
Gluconacetobacter.
NCBI_TaxID=28448;
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Valla S.;
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Pubmed-8083166;
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STRAIN-ATCC 53582;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstarion the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                         DOMAIN: There are two conserved domains in the globular part of the catalytic subunit: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the OXXRW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain in the active site.

INDUCTION: Cellulose is produced at a linear rate with respect to
                                                                                                                                                                                                                                                                                              Saxena I.M., Brown R.M. Jr., Fevre M., Geremia R.A., Henrissat B.; "Multidomain architecture of beta-glycosyl transferases: implications
                                                                                                                STRUCTURE MODELING, AND MUTAGENESIS OF D-188; D-189; D-236; D-333
                                binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE ACSB/BCSB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: Was originally (Ref.1) thought to be two separate ORFs named acsA and acsB, due to a frameshift in position 678.
                                                 the
            Lin F.C., Brown R.M. Jr., Drake R.R. Jr., Haley B.E.;
"Identification of the uridine 5'-diphosphoglucose (UDP-Glc)
subunit of cellulose synthase in Acetobacter xylinum using th
photoaffinity probe 5-azido-UDP-Glc.";
J. Biol. Chem. 265:4782-4784(1990).
                                                                                                                                                                                                synthase:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell growth when O(2) is present.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cellulose biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                              Saxena I.M., Brown R.M. Jr., Dandekar T.;
"Structure-function characterization of cellulose
relationship to other glycosyltransferases.";
Phytochemistry 57:1135-1148(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR003919; Cellsynth_A.
InterPro: IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
PRINYS; PR01433; CELLSNTHASEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X54676; CAA38487.1; ALT_FRAME.
EMBL; X54676; CAA38488.1; ALT_FRAME.
EMBL; M96060; AAA16971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane.
                                                                                                                                                                                                                                                                ON DOMAIN ARCHITECTURE
                                                                                                                              Q-369; R-370 AND R-372.
STRAIN-ATCC 23769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     741
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PIR; S13732; S13732
                                                                                                                                                              PubMed-11430986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
                                                                                                                                                                                                                                                                REVIEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                394 SDDGASMLTFDALAETSEFARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDR 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 EQIG------GFATQTVTEDAHTALKMQRLGWSTAYL--RIPLAGGLATERLI 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 LHIGORVRWARGMLQI-FRIDNPL---FGRGLSWGORLCYLSAMTSFLFAVPRVIFLSSP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     874 AICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVG----IDEWWRNEQFW-V 928
                                                                                                                                                                                                                                                                                                                                                                    280 VLRLVVLSIFLHYRLTNPVRNAYPLWL-----LSVICEIWFALSWILDQFPKWFPINRE 333
                                                                                                                                                                                                                                                                                                                                                                                         80 VLSGLVSLRYLTWRLTETL -- SFDTWLQGLLGTMLLVAELYALMMLFLSYFQTIAPLHRA 137
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574 REAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFFDINLRGLDGIQGPVYVGT
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                                                                                                                                                                                                                                                                                                                                Pred. No. 3e-06;
88; Mismatches 245; Indels 298;
                                                                                                                                                             SUBSTRATE BINDING (POTENTIAL).
B-SUBSTRATE BINDING (POTENTIAL).
D->N: DECREASE IN ACTIVITY.
D->P: LOSS OF ACTIVITY.
D->Y: LOSS OF ACTIVITY.
D->X: LOSS OF ACTIVITY.
D->X: LOSS OF ACTIVITY.
D->X: LOSS OF ACTIVITY.
D->X: LOSS OF ACTIVITY.
C->M: LOSS OF ACTIVITY.
C->M: LOSS OF ACTIVITY.
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                                                                                                                                                                                                                                                                                             63AB8952BC39E961 CRC64;
                                                                                                                                                                                                                                                                      DECREASE IN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 LDDG-----RRPEF-----
                                                                                                                                                                                                                                                                                    LOSS OF ACTIVITY
        SUBDOMAIN A. SUBDOMAIN B.
DI-GMP BINDING
                                                                                                                                                                                                                                                                                                                      Score 207;
          CATALYTIC
                                                        POTENTIAL. POTENTIAL.
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Matches 154; Conservative
                                  1550 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                     COFFACTOR: Magnesium (89 similarity).
ENZYME REGULATION: Activated by bis-(3'-5') cyclic diguanylic acid (cd1-GMP) (By similarity).
PATHWAY: Bacterial cellulose biosynthesis.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: There are two conserved domains in the globular part of the catalytic subunit: the N-terminal domain (domain A) contains the conserved DXD motif and is possibly involved in catalysis and substrate binding. The C-terminal domain (domain B) contains the OXXW motif and is present only in processive glycosyl transferases. It could be involved in the processivity function of the enzyme, possibly required for holding the growing glycan chain
                                                                           NMVGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGL-MGRQ------NRTP 1040
                                                 VYETTMALFLVRVTIVTLLSPSRGKFNVTDKGGLLEKGYFDLG-----AVYPNIILGL 520
                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cellulose synthase 1 catalytic subunit [UDP-forming] (EC 2.4.1.12).
                                                                                                                                                                                                                                                                                                                                                                                                               Umeda Y., Hirano A., Ishibashi M., Akiyama H., Onizuka T., Ikeuchi
                                                                                          -----AASPLALLAYAIPHM-FHAVGTASKINKGWR-YSFWSE
                        IGGISAHLFAVFQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILI
                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
Gluconacetobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR003919, Cellsynth_A.
InterPro: IPR001919, Cellsynth_A.
InterPro: IPR001173; Glycos_transf_2.
Pfam; Pr00535; Glycos_transf_2, 1.
PRIMTS; PR01499; CELLSWTHASEA.
Cellulose blosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                      745 AA
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PubMed-10382968;
                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                               Acetobacter xylinus
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=28448;
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                                                                                                                            1041 TIVIV 1045
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Q9WX61;
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                                                                                                                                                                                                                                                                                                                      IVDPLKEPPIVTANTVLSILAVDYPVDKVSCYV 393
                                                                                                                                                                                                                                                                                                                                                                      KKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDR 453
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                                                                                                                                                                                                                                              Indels 319;
                                                                                                                                                                                                                      Length 745;
                                                                                                                                                          ENTIAL.
SSTRATE BINDING (POTENTIAL).
SSTRATE BINDING (POTENTIAL).
           Α̈́ H
         SUBDOMAIN
                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                               238;
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No. 2.1e-06;
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                                                                                     01-AUG-1990 (Rel. 15, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bacillopetidase F precursor (EC 3.4.21.-) (Esterase) (RP-I protease)
BPR OR PDF.
                                                                                                                                                                                                                                                                                                                        STRAIN=168;
MEDLINE-90368623; PubMed-2118514;
Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 195-222.
MEDLINE-90170864; PubMed-2106512;
Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
                                                                                                                                                                                                                                                                  "Bacillopeptidase F of Bacillus subtilis: purification of the protein and cloning of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90216713; PubMed-2108961; Wu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.; "Cloning, genetic organization, and characterization of a structural gene encoding bacillopeptidase F from Bacillus subtilis."; J. Biol. Chem. 265:6845-6850(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-168 / Marburg;
MaDLINE-20174995; PubMed-2106671;
Masuda E.S., Anaguchi H., Sato T., Takeuchi M., Kobayashi Y.;
"Nucleotide sequence of the sporulation gene spoiiGA from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beall B., Lowe M., Lutkenhaus J.;
"Cloning and characterization of Bacillus subtilis homologs of Escherichia coli cell division genes ftsZ and ftsA.";
J. Bacteriol. 170:4855-4864(1988).
                                                                                                                                                                                       Bacillus
                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae;
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Bacteriol. 172:1470-1477(1990).
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MEDLINE-89008108; PubMed=3139638;
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                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558 AEDNVSVTSVKLSYKLDOGEWTEITAKRISGDHLKGT-----YQAEIPDIKGTKLS 608
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A -> V (IN REF. 3).

KHOMA -> W (IN REF. 3).

QPOVLP -> RTRAIXS (IN REF. 3).

AQVSVVETG -> FCRSRHKSV (IN REF. 3).
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96; Mismatches 314; Indels
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19.8%; Pred. No. 4
email to license@isb-sib.ch)
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InterPro; PR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
PROSITE; PS00135; SUBTILIASE_ASP; PP
PROSITE; PS00137; SUBTILASE_ASP; PP
PROSITE; PS00138; SUBTILASE_SER; 1.
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                           EMBL; M29935; AAA62679.1; --
EMBL; J05400; AAA83362.1; --
EMBL; M22630; AAA2458.1; --
EMBL; X17344; CAA35224.1; --
EMBL; Z99111; CAB13403.1; --
EMBL; Z99112; CAB13404.1; --
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M22630; AAA22458.1;
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299111; CAB13404.1;
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PIR; A36734; A36734.
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_plant:*
sp_rodent:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rvirus:*
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sp_fungi:*
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sp_invertebrate:*
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Database :

	Description		Q911i1 zea mays (m	Q911i6 zea mays (m	Q911i5 zea mays (m	d muiqyssog 3xgx60		048948 arabidopsis	Q91118 zea mays (m		048946 arabidopsis	Q91112 zea mays (m	Q91114 zea mays (m	•••	Q9sww6 arabidopsis	Q9xhp6 arabidopsis	Q9skj5 arabidopsis	Q9fnc3 arabidopsis
SUMMARIES	ID		Q9LL11	91776Ö	Q9LLI5	9x9x6ō	Q9FHK6	048948	Q9LLI8	09LLI9	048946	Q9LL12	09LLI4	Q9LLI3	O9SWW6	9днх60	Q9SKJ5	Q9FNC3
	DB	;	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	% Query Match Length DB		1079	1077	1076	1067	1065	1065	1074	1075	1081	1094	1059	1086	1026	1026	1065	1043
	% Query Match		93.9	93.8	89.0	79.2	78.4	78.0	69.1	68.8	9.89	66.5	66.1	66.1	65.8	65.7	65.4	64.8
	Score		5423.5	5421.5	5143	4577.5	4530	4507	3993.5	3981	3963.5	3844.5	3820	3818	3801	3795	3778.5	3746
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Gaps

93.9%; Score 5423.5; DB 10; Length 1079; ilarity 92.2%; Pred. No. 0; Conservative 46; Mismatches 37; Indels 1;

Query Match Best Local Similarity Best Local Sim Matches 996;

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61 CLOCKTKYKRHRGSPAIRGEEGDDTDADDGSDENYPASGTEDOKQKIADRWRSWRWNTGG 120

1 MDGDADALKSGRHGAGDVCQICADGLGTTLDGDVFTACDVCRFPVCRPCYEHERKEGTQA 60

Ogav71 oryza sativ Og3xq1 nicotiana a Og947 arabidopsis Og1fd9 populus x c O65338 arabidopsis Og572 arabidopsis Og9117 zea mays (m P93155 gossypium h Ogaxk0 zinnia eleq ORW1W0 gossypium h Og528 arabidopsis Og1368 populus tre Og5738 arabidopsis Og9433 arabidopsis Og9433 arabidopsis Og9439 arabidopsis Og9xya sativ Og9x19 arabidopsis Og9xya arabidopsis	MENTS	### 1079 AA. ed) sequence update) annotation update) annotation update) phyta: Embryophyta: Tracheophyta: lopsida: Poales: Poaceae; PACC clade: is T., Dhugga K.S., is T., Dhugga K.S., int. int. int.
099AV71 048947 048947 09FGF9 09FGF9 081649 095338 095338 095338 091368 091368 091368 0993156 0998137 0998136 0998136 0998136 0998136 0998136 0998136 0998136 0998136	ALIGNMENTS	PRT; 1079. 15, Created) 15, Last sequence 21, Last annotati 15, Last annotati 15, Last annotati 15, Last annotati 16, Last annotati 17, Cast annotati 18, Streptophyta, E 18, P. F. 19, P. F. 11324(2000) 11, P. F. 11056_Synt. 11, P. F. 12, P. F. 12, P. F. 12, P. F. 12, P. F. 13, P. F. 14, P. F. 15, P. F. 16, P. F. 17, P. F. 18, P. F. 18, P. F. 19, P. F. 1
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01-JUP	CESA-4 Zea ma Eukary	Sperme Panico NCBI_1	MEDLII HO1la	"A COI family Plant EMBL:	Interl Interl Pfam;	SMART	Query Mai Best Loca Matches		-	61 (61	121	119	181	179	241	239	301	299	361	359	421	419	481	479	541	539	601	599	661
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61 CPQCKNKYKRHKGSPAIRGEEGDDTDADDASDFNYPASGNDDQKQKIADRMRSWRMNAGG 120	121 SGNVGHPKYDSGEIGLSKYDSGEIPRGYVPSVTNSOMSGEIPGASPDHHMASPTGNISRR 180 :	181 AFFPYVNHSPNPSREFSGSIGNVAWKERVDGWKMKQDKGAIPMTNGTSIAPSEGRAATDI 240 	241 DASTEYNMEDALLNDETRQPLSRKVPIASSKINPYRMVIVLRIFVLHYRLTNPVRN 300 	301 AYPLWLLSVICEIWPALSWILDOFPKWFPINRETYLDRLALRYDREGEPSOLAAVDIFVS 360	TVDPLKEPPIVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFDALAETSEFARKWVPFV 4	361 TVDPMKEPPLVTANTVLSILAVDYPVDKVSCYVSDDGAAMLTFDALAETSEFARKWVPFV 420	421 KKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVSKALKVPEE 480 	481 GWIMODGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAG 540 401 [401 GWIMYDOLFWEGUNIENDIEGHEGHEYFEDHEGGEDIEGHEFEN FYSKEKKESTEYNGON 641 AMMATUDUGAUTHUGOVWENIENTOCHYTUNGKAUPEAMFELMDULZDOVYVVORDORFD	541 AMMININGSANTHOCHTAIN TO THE	O41 RUMALNYONYLINOQIMINALOONITIENOONIT	001 IDKNDKYANNATVEFDINLKGLDG.LGGVVYVGTGCVVNRAIKGTEPIARAKCFEFLAGA.000	661 CGGKKKASKSKKRSSDKKKSNKHVDSSVPVFNLEDIEEGVEGAGFDDEKSVLMSOMSLEK	661 CGGRKKGSKSKK-GSDKKKSQKHVDSSVPVFNLEDIEEGVEGAGFDDEKSLLMSQMSLEK	721	720 RFGOGAAFVASTIMEVGCVPOSATPESTLKEAIHVISCGXEDKIEWGTEIGWIYGSVTED	781 TITGERMHARGWRSVYCMPKRDAFKGSAPINISDRINOVIRWALGSVEILFSSRHCPLWYG 84	780 ILTGERMHARGWRSTYCMPRIPERSSAPINISDRINOVLRWALGSVELLESBECPLWYG		841 IGGKLAKTLEKRAIINTIITTITTILLELLIVILLEKILLELIGARIAMETARELISNIASIAKILEK 	001 TAYAR AN TANAHARAN MANAKAN	901 SIFATGILEMENSOGOILEMENNENELEMENTOGOISANDE AVEQUELANTALANTENETATIONA 900	961 NDEECDFAELYMFKWITT.I.PDTTII.I.INWV.VVAGTSYAINSGYOSW.DF.FGRIFFAEW		900 SDEDGDFAELIMFKWITLLIFFITTLINLYGVYAGISTALNSGIQSMGFLFGALFFAFW I	1021 VIVHLYPFLKGLMGRQNRTPTIVIVWAVLLASIFSLLMVRVDFFTRLAGFNIQTGCINC 108	1020	SULT 2	DLLO Q9LLI6 PRELIMINARY; PRT; 1077 AA.	DT 01-0CT-2000 (TrEMBLrel. 15, Created) DT 01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
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Ophyta; Embryophyta; Tracheophyta;
Liopsida; Poales; Poaceae; PACC clade;
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Lant cellulose synthase (CesA) gene
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annotation update)
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No. 0;
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LINE-2039328; Pubmed-10.
land N., Holland D., Hel.
onostle-Cazares B., Delm
comparative analysis of
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matophyta; Magnoliophyt
coideae; Andropogoneae;
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                               IDASTEYNMEDALLNDETRQPLSRKVPIASSKINPYRMVIVLRLVVLSIFLHYRLTNPVR
                                                                      NAYPLWLLSVICEIWFALSWILDQFPKWFPINRETYLDRLALRYDREGEPSQLAAVDIFV
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2002 (TEMBLE). 21, Last sequence update)
Cellulose synthase-5.
CESA-5.
Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Panicoideae; Andropogoneae; Zea.
NCBL_TAXID-4577;
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 CGGRKKASKSKK-GSDKKKSQKHVDSSVPVFNLEDIEEGVEGAGFDDEKSLLMSQMSLEK
                               ILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYG
                                                                      VIVHLYPFLKGLMGRQNRTPTIVIVWAVLLASIFSLLWVRVDPFTTRLAGPNIQTCGINC
                                                                                                                                           SIFATGILEMRWSGVGIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKA
                    RFGQSAAFVASTLMEYGGVPQSSTPESLLKEAIHVISCGYEDKSEWGTEIGWIYGSVTED
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Holland N., Holland D., Helentjaris T., Dhugga K.S.,
Xoconostle-Cazares B., Delmer D.P.;
"A comparative analysis of the plant cellulose synthase
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E 1076 AA; 120724 MW; 41EE7C20EDA54F27 CRC64;
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87.6%; Pred. No. 0;
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EMBI, AF20029; ARF89965.1; .
InterPro: IPR005150; Cellulose_synt.
InterPro: IPR001841; Znf_ring.
Fram: PF03552; Cellulose_synt: 1.
SEQUENCE 1076 AA; 120724 MW; 41EE7
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SEQUENCE FROM N.A.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
Cellulose synthase catalytic subunit.
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RESULT (048948 ID 048

	Db 120GNGKGPEWQ	173	DD 1/4 FISSIVDESVE OV 231 PSEGRAATDID	227	291	Db 285 QYRISHPVRNA	Qy 351 QLAAVDIFVST	Db 345 QLAPIDVFVST	Oy 411 EFARKWVPFVK	Qy 471 VSKALKVPEEG			591	DD 585 YVQFPQRFDGI	Qy 651 AKKPGFLAS : : Db 645 EADLEPNIVVK	Qy 709 KSVLMSQMSLE	: Db 702 RSVLMSQRKLE	Qy 769 EIGWIYGSVTE	Db 762 EIGWIYGSVTE	Qy 829 ILFSRHCPLWY	DD 822 ILLSRHCPIWY	Qy 889 NLASIWFIALF	DD 882 NYAGMFFILLE	Qy 949 GIDINFTVISK	DD 942 GIDINFIVISK	Qy 1009 GPLFGKLFFAF	DD 1002 GPLFGKLFFSI	QY 1066 TRLAGPNIQTC	Db 1062 QKAAALGQC	RESULT 8 Q9LLI9 TD OGILIG PREL	AC Q9LLI9; DT 01-OCT-2000 (TrB
DD 599 DINLRGLDGIQGPVYVGTGCVFNRTALYGYEPPIKVKHKKPSLLSKLCGGSRKKNSKAKK 658	674 SSDKKKSNKHVDSSVPVFNIEDIEBGVEGAGFDDEKSVIMSOMSLEKRFGOSAAFVASTI.	659 ESDKKKSGRHTDSTVEVFNLDDIEEGVEGAGFDDEKALLMSQMSLEKRFGQSAVFVASTL	Qy 734 MEYGCVPQSSTPESLLKEAIHVISCGYEDKSEWGTEIGWIYGSVTEDILIGEKMHARGWR 793	Db 719 MENGGVPPSATPENLLKEAIHVISCGYEDKSDWGMEIGWIYGSVTEDILTGFKMHARGWR 778	794 SVYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAY	SIYCMPKLPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPIWYGYNGRLKFLERFAY	OY 854 INTITYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWS 913	039 VNIIITELISIELEMIICIPERAVCEETINGETIEVATAN ENSEENSEENSEENSEENSEENSEENSEENSEENSEEN	OY 914 GVG.LDEWARRECEWVIGGLEARLEAVEQGLILKVILAGITINETYTSRANDEGEOFAELINE 973 DD 899 GVGIDEWARNEQFWVIGGVSAHLFAVFQGILKVLAGIDINFTVTSRASDEDGDFAELXLF 958	Qy 974 KWTTLLIPPTILIINMVGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLM 1033	Db 959 KWTTLLIPPTTLLIVNLVGVVAGVSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLM 1018	Qy 1034 GRONRTPIIVIVWAVLLASIFSLLWVRVDPFTTRLAGPNIQTCGINC 1080		ID Q9LLI8 PRELIMINARY; PRT; 1074 AA. AC OGTITA.	DT 01-0CT-2000 (TrEMBLrel. 15, Created) DT 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) DT 01-1UN-2002 (TrEMBLrel. 21, Last annotation update)	DE CELLUIOSE SYNCHASE'Z. GN CESA-2	a mays (Maize). .karyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OC Spermatophyta; Magnollophyta; Lillopsida; Foales; Foaceae; FACC Clade; OC Panicoideae; Andropogoneae; 2ea. OX NCRT TextD=4477:	NN [1]	RX MEDITINE=20398328 PubMed=10938350;	Octoboxile-Cazaris D., neterioratis 1., Diugga N.S., Octoboxile-Cazaris D., Delmer D.P.;	nmily."; mily."; mily.";	KL FIGHT FMYSIO1. 123:1213-1224(2000). DR EMBL; AF200526; AF8P896521; DR TALCADA. TUDOACIEN. OF 1.1.0.0	DR INCEPRO) IFROUGLOU CELLULOSE_SYNC. DR INCEPRO; IPROUGLY, CELLULOSE_SYNC.	AART; SM00184; RING; 1.	EQUENCE 10/4 AA; 12118/ MW; A116E66FU364E210 CE		MACCHES 149; CONSTANTANTOLIVE 154; MISSIGACCHES 155; INGELS 59; Gaps	29 LOGDROW LANGUAGOVICACADOLITADOVETATOVACETE VERCETERRANDOVETA OVER THE STANDARD OVER THE SANGOVICACOTOGOTIVACETE STANDARD STAND	Qy 61 CLQCKTKYKRHRGSPAIRGEEGDDTDADD-GSDFNYPASGTEDQKQKIADRMRSWRMNTG 119 	120 GSGNVGHPKYDSGEIGLS-KYDSGEIPRGYVPSVTN-SQMSGEIPGASPDHH-MMS 17

1008 1065 888 948 941 530 590 650 828 290 350 SILAVDYPVDKVSCYVSDDGASMLTFDALAETS 410 IDYLKDKVQPSFVKDRRAMKREYEEFKIRINAL 470 708 768 821 881 344 464 524 584 644 701 284 RQPLSRKVPIASSKINPYRMVIVLRLVVLSIFL **HECHIQVELCHSGGLDTEGNELPRLVYVSREKR** DKKKSNKHVDSSVPVFNLEDIEEGVEGAGFDDE SSYIMKRTESSAPIFNMEDIEEGIE--GYEDE SYGGVPQSSTPESLLKEAIHVISCGYEDKSEWGT YCMPKRPAFKGSAPINLSDRLNQVLRWALGSVE TTIYPLTSLPLLVYCILPAICLLTGKFIMPEIS GIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLA QNRTPTIVIVWAVLLASIFSLLWVRVDPF---T GSIGNVAWKERVDGWKMKQDKGAIPMTNGTSIA NLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIK ::| |||||:|::|||| ::||
XGLNSVDWKERVESWRVKQDKNMLQVTN----RT; 1075 AA. ted) rediltgekmhar ||||||||||||||| |EDILTGEKMHAR SKANDEEGDFAEI |||:||:|||| SKASDEDGDFAEI | :: | OLQGDDADLSSS DASTEYNMEDAL KKYDIEPRAPEE PFPYVNHSPNPS ||::||||||| GWIMQDGTPWPC AMNALVRVSAVI IDRNDRYANRN || :|||||||| IDLHDRYANRN KSCCGRRK-RK YGYGGRLKFLE ||| ||| || YGYNGRLKLLE! FLSIFATGILE | |||||||||| FASIFATGILE EMBLrel. 15 PVPV--RIVDP SLCGGKKKASK EKRFGQSAAFV FWVIVHLYPFL E-GTGSNGEDM AYPLWLLSVIC ||||||||| EKRFGQSPIFI ||||:||||| ||:|| |CGVNC 1074 CGINC 1080 SLIMINARY;

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KLFFAFWVIVHLYPFLKGLMGRQNRTPTIVIVWAVLLASIFSLLWVRVDPF---TTRLAG 1070
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 HCPLWYGYGGRLKFLERFAYINTTIYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASI 893
                                                    FTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINWVGVVAGTSYAINSGYQSWGPLFG
                                       SQMSLEKRFGQSAAFVASTLMEYGGVPQSSTPESLLKEAIHVISCGYEDKSEWGTEIGWI
                                                                                         YGSVTEDILTGFKMHARGWRSVYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSR
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Teryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R. De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Hoheisel J., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=98111412; PubMed=9445479;
Arioli T., Peng L., Betzner A.S., Burn J., Wittke W., Herth W.,
Camilleri C., Hofte H., Plazinski J., Birch R., Cork A., Glover
Redmond J., Williamson R.E.;
"Molecular analysis of cellulose biosynthesis in Arabidopsis.";
Science 279:717-720(1998).
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Cellulose synthase catalytic subunit.
RSWI OR F8B4.110 OR AT4G32410.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea.
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 sequence update)
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Best Local Similarity 68.5%; Pred. No. 1.1e-313;
Matches 747; Conservative 132; Mismatches 163;
                                                                                                                                                     Dhugga
                                                                                                                                       MEDLINE-20398328; pubMed=10938350;
Holland N., Holland D., Helentjaris T.,
Xoconostle-Cazares B., Delmer D.P.;
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EMBL, AF200525; AAF89961.1; -.
InterPro; IPR005150; Cellulose_synt.
InterPro; IPR001841; Znf_ring.
Pfam; PF03552; Cellulose_synt; 1.
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SEQUENCE 1075 AA; 121181 MW;
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                        Cellulose synthase-1.
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                                                  mays (Maize)
                                                                                                  NCBI_TaxID=4577;
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15; cophyta; Embryophyta; Tracheophyta; Lliopsida; Poales; Poaceae; PACC clade; RNEQEWVIGGISAHLFAVFOGLLKVLAGIDTNF 954 :| :| :| :| :| | :| | | :| | | :| | | :| | | :| | | :| | | | :| | | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | VPSVTNSQMSGEIPGASPDHHMMSPT----G 175 GSDFN-YPASGTEDQKQKIADRMRSWRMNTGGS 121 FSG-SIGNVAWKERVDGWKMKQDKGAIPMTNGT 227 69; Gaps io; Aris T., Dhugga K.S., P.; Jant cellulose synthase (CesA) gene od. No. 1.4e-302; Mismatches 175; Indels 69; (DFBBC18F49D23F5E CRC64; sequence update) annotation update) T; 1094 AA. ted) ynt.

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Zesa mays (Maize).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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MEDLINE-20398328; PubMed=10938350;
Holland N., Holland D., Helentjaris T., Dhugga K.S.,
Xoconostle-Cazares B., Delmer D.P.;
"A comparative analysis of the plant cellulose synthase (CesA) gene
                                                                                          P-KTKKRPSRTCNCWPKWCLSCCCSRNKNKKRTTKPKFEKKRELFFKRAENPSPAYALGE
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EPSQLAAVDIFVSTVDPLKEPPIVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFDALA
                                                          EKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYINNSKAVREAMCFLMDPNLGP
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                                             ETSEFARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRI
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                                                                   289DA26B25232249 CRC64;
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                                                                                     Score 3820; DB 10;
Pred. No. 1.3e-300;
10; Mismatches 168;
family.";
Plant Physiol. 123:1313-1324(2000).
EMBL, ARZ00530, AAF89966.1;
InterPro; IPR005150; Cellulose_synt.
InterPro; IPR01841; Znf_ring.
Pfam: PF03552; Cellulose_synt; 1.
SMART; SM00184; RING; 1.
SEQUENCE 1059 AA; 120044 MW; 289DA;
                                                        SM00184; RING; 1.
CE 1059 AA; 120044 MW;
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                                                                  GNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYV 525
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Ntophyta; Embryophyta; Tracheophyta;
Nudicotyledons; core eudicots; Rosidae;
Nicaceae; Arabidopsis.
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tler S., Somerville C.R., Turner S.R.;
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 cellulose
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Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF091713; AAD40885.1; ...
EMBL, AL3914142; CAC01737.1; ...
InterPro; IPR005150; Cellulose_synt.
InterPro; IPR001841; Znf_ring.
Pfam; PF03552; Cellulose_synt; 1.
SWART; SMO0184; RING; 1.
SEQUENCE 1026 AA; 115797 MW; 503BFBC78BE6E511 CRC64;
                     synthesis.";
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"The irregular xylem3 locus of Arabidopsis encodes synthase required for secondary cell wall synthesis Plant Cell 11:769-780(1999).
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                                                                        SEQUENCE FROM N.A.
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Matches 725;
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                                                                                                      735 CRGWRSIYCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEIFFSRHSPLWYGYKGGKLKW 794
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN—CV. LANDSBERG ERECTA;
STRAIN—S9264300; PubMed=10330464;
MEDLINE-99264300; PubMed=10330464;
Taylor N.G., Scheible W.R., Cutler S., Somerville C.R., Turner Taylor N.G., Scheible W.R., Cutler S., Somerville C.R., Turner The irregular xylem3 locus of Arabidopsis encodes a cellulose synthase required for secondary cell wall synthesis.";
Fhant cell 11:769-780(1999).
EMBL; AF088917; AAD32031.1; -.
InterPro; IPR001841; Znf_Ling.
InterPro; IPR001841; Znf_Ling.
Pfam; PR03552; Cellulose_synt; 1.
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llarity 67.5%; Pred. No. 1.3e-298;
Conservative 104; Mismatches 157;
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01-NOV-1999 (TrEMBLrel. 12, Last seq
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es 724; Conserv
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	R R R R R		RL N. RN []			one	Hest Matcl	ag Oy	qa o	Db	qa	d Q	qa	δδ	ag Ad	qq qq	γo	qu	Oy	oy y	qa
7 253 LNDETROPLSRKVPIASSKINPYRMVIVLRLVVLSIFLHYRLTNPVRNAYPLMLLSVICE 312 	7 313 IMPALSWILDQFPKWFPINRETYLDRIALRYDREGEPSQLAAVDIFVSTVDPLKEPPIVT 372 	7 373 ANTVLSILAVDYPVDKVSCYVSDDGASMLTFDALAETSEFARKWVPFVKKYDIEPRAPEF 432 	433 YFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIRINALVSKALKVPEEGWIMQDGTPWPG 492 	4 93 NNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVL 552	553 TNGQYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNT 612 1	/ 613 VFFDINLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKKPGFLASLCGGKKKAS 668	669 KSKKRSSDKKSNKHVDSSVPVFNLEDIEEGVEGAGFDDEKSVLMSOMSLEKRFGQSAAF 728 1	729 VASTLMEYGCVPQSSTPESLLKEAIHVISCGYEDKSEWGTEIGWIYGSVTEDILJGFKMH 788	7 789 ARGWRSVYCMPKRPAFKGSAPINLSDRLNOVLRWALGSVEILFSRHCPLWYGY-GGRLKF 847 	y 848 LERPAYINTIYPLISLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFLSIFATGI 907 	9 908 LEMRWSGVGIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKANDEEGDF 967 :	y 968 aelymekwttlidpttilinmvgvvagtsyainsgygsmgplegklefaewivhlyp 1027 - - - - - - - - - - - - -	1028	974	SSULT 15 SK15	OSSKJS PRELIMINARY; PRT; 1065 AA.	OT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) DT 01-LIN-2002 (TrEMBLrel 2) 11 Last annotation undate)	Putative cellulose synthase catalytic subunit.	Arabidopsis thaliana (Mouse-ear cress). Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,	<pre>Permacucing II magnolloping at enticolyteuons; core entic eurosids II; Enassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702;</pre>	N [1] P SEQUENCE FROM N.A.
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Shea T.P., Benito M.-I., Town C.D., J.L., Barnstead M.E., Feldblyum T.V., J., Ronning C.M., Koo H., Moffat K.S., E., Gwaydm L., Tallon L.J., Gill J.E., T.H., Goodman H.M., Somerville C.R., man W.C., White O., Elsen J.A.,
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DDARLPMSRVVHFPSARMTPYRIVIVLRLIILG 273
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|-----VSGEIP--TPDRNATLSP
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F2AE36C9492A6076 CRC64;
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STRAIN-CV. COLUMBIA;
MEDLINE-20083487; Pubmed-1C
Lin X., Kaul S., Rounsley 9
Eujii C.Y., Mason T.M., Bow
Buell C.R., Retchum K.A., F
                                                                                Cronin L.A., Shen M., VanAl
Adams M.D., Carrera A.J., C
Copenhaver G.P., Preuss D.,
Salzberg S.L., Fraser C.M.,
"Sequence and analysis of c
thaliana.";
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Submitted (MAR-2000) to the
EMBL, AC006300; AAD20713.1,
InterPro; IPR005150; Cellul
InterPro; IPR001309; ICE_PZ
InterPro; IPR001841; Znf_rS
                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03552; Cellulose_S
SMART; SM00184; RING; 1.
PROSITE; PS01121; CASPASE_S
SEQUENCE 1065 AA; 12061
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Search completed: February 19, 2003, 16:36:55 Job time: 63 secs

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Patent No. 6271443

GENERAL INFORMATION:
APPLICANT: Stalker, D. et al.
TITLE OF INVENTION: Plant Cellulose Synthase and Promoter
TITLE OF INVENTION: Pageuences
FILE REFERENCE: 15621/01/US
CURRENT APPLICATION NUMBER: 06/029,987

PRIOR APPLICATION NUMBER: 60/029,987

PRIOR FILING DATE: 1996-10-29
NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 881
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US-08-268-161A-95
US-08-45-702A-95
US-09-639-639-95
PCT-US93-12588-95
PCT-US93-12588-95
PCT-US93-12588-95
US-08-45-274B-103
US-08-45-95A-103
US-08-45-95A-103
US-09-099-639-103
PCT-US95-08071-103
US-08-45-260-2
US-08-461-503-2
US-08-461-503-2
US-08-461-503-2
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US-08-461-503-2
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93.4%; Pred. No. 0;
tive 39; Mismatches
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823; Conserv
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    Query Match
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(c) 1993 - 2003 Compugen Ltd
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US-07-925-695-5
US-09-134-001C-4051
US-07-998-003A-95
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US-08-960-048-12
US-07-689-008-2
US-08-960-048-10
US-08-960-048-10
US-08-110773-4
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S-08-669-656A-2
S-08-590-554A-6
S-08-184-223-6
S-08-620-717A-9
S-08-620-773-6
S-08-119-773-6
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Listing first 45 summaries

    protein search, using sw model

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197	Oy 257 TROPLSRKVPIASSKI. 1 1 1 1 1 1 155 S-QPLZIIPIPKSRL. Oy 317 LSWILDOFPKWPFINR		274	334	394		677	736 628 796	Db 688 YCMPLRPAFKGSAPIN Qy 855 NTTIYPLTSLPLLVYC Db 748 NTIYYPFTSLPLIAYC	Oy 915 VGIDEWWRNEOFWVIGG	Qy 975 WTTLLIPPTILLINM	Qy 1035 RQNRTPTIVIVWAVLLA : : Db 927 RQNRTPTIVVLWSVLLA	RESULT 3 US-08-960-048-7 : Sequence 7, Application U	; FALCHIL NO. 02/1443; GENERAL INFORMATION: APPLICANT: Stalker, D. TITLE OF INVENTION: Pla	; TITLE OF INVENTION: Sec ; FILE REFERENCE: 15621/(; CURRENT APPLICATION NUM ; CURRENT FILING DATE: 19 ; PRIOR APPLICATION NUMBER
		POSSTPESLLKEAIHVISCGYEDKSEWGTEIGMIYGSVTEDILTGFKMHARGWRSVYCMP	800 KRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTTIY 859 	860 PLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVGIDE 919 : : :	920 WWRNEGFWYIGGISAHLFAVFQGLLKVLAGIDTNFTYTSKANDEEGDFAELYMFKWTTLL 979 	980 IPPTILLIINNVGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLMGRQNRT 1039 	1040 PTIVIVWAVLASIESLLWVRVDPFTTRLAGPNIQTCGINC 1080 : :	ESULT 2 S-08-960-048-6 Sequence 6, Application US/08960048C Patent No. 627143 GENERAL INFORMATION: APPLICANT: Stalker, D. et al.	; TITLE OF INVENTION: Plant Cellulose Synthase and Promoter; TITLE OF INVENTION: Sequences; FILE REFERENCE: 15621/01/US ; CURRENT APPLICATION NUMBER: US/08/960,048C ; CURRENT FILING DATE: 1997-10-29	PRIOR APPLICATION NUMBER: 60/029,987 PRIOR FILING DATE: 1996-10-29 NUMBER OF SEQ ID NOS: 12 SOFTWARE: FastSEQ for Windows Version 4.0	SENCTH: 974 TYPE: PRT PRGANIEW GOSSYPIM hirsutum	Ouery Match Query Match Best Local Similarity 61.5%; Score 3477; DB 4; Length 974; Best Local Similarity 61.5%; Pred. No. 1.9e-318; Matches 657; Conservative 129; Mismatches 176; Indels 106; Gaps 15;	18 VCQICADGLGTTLDGDVFTACDVCRFPVCRPCXEHERKEGTQACLQCKTKYKRHRGSPAI 77	78 RGEBEODDTDADDGSDFNYPASGTEDQKQKIADRMRSWRMNTGGSGNVG-HPKYDSGEIGL 136	137 SKYDSGEIPRGYVPSVTNSQMSGEIPGASPDHHMMSPTGNISRRAPFPYVNHSPNPSREF 196 1
ga V	Db Qy Db	Oy Dp	o d	Oy Dp	Qy Db	Qy Dp	Oy 1	RESULT US-08-9 ; Seque ; Paten ; GENER	HILL	NON		Query M Best Lo	Oy Db	Qy Db	oy Op

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                                                                                                              24;
                                                                                         Length 685;
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GENERAL INFORMATION:

APPLICANT: Stalker, D. et al.

TILLE OF INVENTION: Sequences

FILE REFERENCE: 15621/01/US

CURRENT APPLICATION NUMBER: 1957-10-29

CURRENT FILING DATE: 1997-10-29
                                                                                         Query Match
48.7%; Score 2811; DB 4;
Best Local Similarity 74.1%; Pred. No. 6.1e-256;
Matches 509; Conservative 78; Mismatches 76;
PRIOR FILING DATE: 1996-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 685
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Patent No. 6271443
                                                  ; TYPE: PRT
; ORGANISM: Gossypium hirsutum
US-08-960-048-7
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                                                                                                                                                                                                                                             Score 268; DB 4;
Pred. No. 4.1e-15;
PRIOR APPLICATION NUMBER: 60/029,987
PRIOR FILING DATE: 1996-10-29
NUMBER OF SEQ ID NOS: 12
SOFWRARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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19.5%; Pred. No. 4
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                                                                                                                                                TYPE: PRT
ORGANISM: Escherichia coli
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Matches 156; Conservative
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436 QKIDYLKDKVQPSFVKDRRAMR
        598 LYEYVQTVHLLPAVVSVIFN
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McCutchen
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California
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                                                                                                                                                                                                                                                                                                                                           Indels 347;
                                                                                                                                                                                                                                                                                                            Length 861;
                                                  APPLICANT: Stalker, D. et al.
TITLE OF INVENTION: Plant Cellulose Synthase and Promoter TITLE OF INVENTION: Sequences FILE REFERENCE: 15621/01/US
FULE REFERENCE: 15621/01/US
CURRENT APPLICATION NUMBER: US/08/960,048C
CURRENT FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/029,987
PRIOR FILING DATE: 1996-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FRASEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                          Ouery Match 4.4%; Score 255.5; DB 4; Best Local Similarity 18.5%; Pred. No. 8.9e-15; Matches 137; Conservative 80; Mismatches 176;
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                                                                                                                                                                                                                                                           ORGANISM: Agrobacterium tumefaciens US-08-960-048-12
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LENGTH: 861
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----AVDIEVSTVDPLKEPPIVTANT 375 LPLPDNVDDWPTVDIFIPTYD---EQLSIVRLT 168 FDALAETSEFARKWVPFVKKYDIEPRAPEFYFC 435 FKIRINALVSKALKVPEEGWIMQDGTPWPGNNT 495 LLSVICEIWFALSWILDQ---FPKWFP---- 329 NUCLEIC ACID SEQUENCES FOR THE IF CELLULOSE SYNTHASE OPERON Indels 335; Length 3031; DB 1; re 238.5; DB 1; id. No. 3.1e-12; Mismatches 232; 008 .24 ter Đ. COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
SOFTWARE: PATENTIN Relea Ben-Bassat, Ari Calhoon, Roger Fear, Anna L Gelfand, David Meade, James H APPLICANT: Wong, Hing APPLICANT: Benziman, Moshe TITLE OF INVENTION: METHOD TITLE OF INVENTION: EXPRES Sequence 2, Application US/076 Patent No. 5268274 3: McCutchen, Do Three Embarcader PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 3
FILING DATE: 12-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 4 APPLICATION NUMBER: US 4 FILING DATE: 23-MAR-1990 ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATI TELEPHONE: (415) 393-200 TELEFAX: (415) 393-2286 TELEX: 340817 MACPAG SFO INFORMATION FOR SEQ ID NO: 2 279 IVLRLVVLSIFLHYRLTNPVRN 112 LLMAELYALYMLFLSYFQTIOF 376 VLSILAVDYPVDKVSCYVSDDG || | :|:| ||| ||| || VLGALGIDWPPDKVNVYILDDG APPLICATION NUMBER: US/C 3031 amino acids 53 LIVALVCVLVFFIVGRGKSRR - INRETY - LDRLALRYDREGEE NAME: Murphy, Lisabeth REGISTRATION NUMBER: 31 SEQUENCE CHARACTERISTICS: FILING DATE: 19910422 CLASSIFICATION: 435 Conservative

Db 191VRPEFEQFAKDCGAL 205	LAAVDIEVSTVDP :
Qy 496 RDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNG 555 Db 206	Db 139LPLPDNVDDWPTVDIFIPTYDEQLSIVRLTVLGALGIDWPPR Qy 396 DGASMLTFDALAETSEFARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQI
556 QYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRIVFF	Db 189 DGVRI
616 DINLRGLDGIQCPVYVGTGCVFNRTAIYGYEPPIKAKKPGFLASLCGGKKKASKSKKRSS	Db 194EFEQFAKDCGAL
DD 2/3 285 OY 676 DKKKSNKHVDSSVPVFNLEDIEEGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFVASTLME 735	214
286PEGNLFYGVIQDGNDFWDATFFGSCAI-	OY 576 AMCFLMDPNLGFDVCYVOFPORPDGIDRNDRYANRNTVFFDINLRGLDGIQQ : :
QY 736 YGGVPQSSTPESLLKBAIHVISCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSV 795	636
Qy 796 YCMPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYIN 855 1 1 1 1 1 1 1 1 1	OY 696 IEEGVEGAGFDDEKSVLMSOMSLEKRFGOSAAFVASTLMEYGGVPQSSTPE
OY 856 TIIYPLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWS 913	-FYGVIQDGND ISCGYEDKSEWGTE
QY 914 -GVGIDEWWRNEQFW-VIGGISAHLFAVFQGLLKVLAGIDFNFTVTSKANDEECDFA 968	GFAVETVTEDAHTALRMQRRGWSTAYLRIP GSVEILFSRHCPLWYGYGGRLKFLERFAYINTIYPLT
969 ELYMEKWITLLIPPTILIINWYGVAGTSXAINSGYQSWGPLFG-KLFREFWIVHLY 511 AIY	Db 369 IGRMRWARGMIGI-FRVDNPMLGRGLKLGGRLCYLEAMTSFFFAIPRI Qy 876 CLITGKFIMPEISNLASIWFIALELSIFATGILEMRWSGVGIDEWWRNF
KGLMGRQNRTPTIVIVWAVLLASI 	425 FLFAGONIIAAAPL 932 ISAHLFAVFQGLLKVLAGIDTNFTV :
RESULT 7 US-08-960-048-10 ; Sequence 10, Application US/08960048C ; Patent No. 6271443	Db 473 TFWALFLVRVTIVTLLFPSKGRFNVTEKGGVLEEEEFDLGATYPNIIFATIN Qy 986LIINMVGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGL-
GENERAL INFORMATION: APPLICANT: Stalker, D. et al. TITLE OF INVENTION: Plant Cellulose Synthase and Promoter INTER OF INVENTION: Sequences	RESULT 8 US-09-147-236-3 ; Sequence 3, Application US/09147236A
FILE REFERENCE: 1562 CURRENT APPLICATION N CURRENT FILING DATE:	; Patent No. 6316251 ; GENERAL INFORMATION: ; APPLICANT: TONOUCHI, Naoto
	; APPLICANT: TSUCHIDA, Takayasu ; APPLICANT: YOSHUNGA, Funihiro · apprirant: ratara, Nack
; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 10.	APPLICANT: HANKSHI, MACALISA ; TITLE OF INVENTION: NOVEL ; TITLE OF INVENTION: NOVEL
.; TYPE: THE CONTROL OF T	; FILE REFERENCE: 053/ULL*OPCI ; CURRENT APPLICATION NUMBER: US/09/147,236A ; CURRENT FILING DATE: 1999-04-08 ; EARLIER APPLICATION NUMBER: PCT/JP97/03633
Score 237.5; DB 4; Length 756; Pred, No. 3.5e-13;	; EARLIER FILING DATE: 1997-10-09 ; NUMBER OF SEQ ID NOS: 12 ; SOFTWARE: Patentin Ver. 2.1
VLRLVVLSIFLHYRLITUPVR-NAYPLWLLSVICEIWFALSWILDQFPKW	; SEQ 1D 00 5 ; LENGTH; 756 ; TYPE: PRT
Db 80 VLSALVSLRYLTWRLTETLDFNTWIQGILGVILLMAELYALYMLESYFQTIQPLHRAP- 138	; ORGANISM: Acetobacter xylinum ; FEATURE: ; OTHER INFORMATION: n at positions 15741 and 15767 may be

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L BETA-GLUCOSIDASE
PVDKVSCYVSD 395
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|PPDKVNVYILD 188
                                          VQPSFVKDRRA 455
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VRP-----193
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----PEGNL-- 292
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---LRREAIES 323
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---YIGRVDVD 213
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                                                            Gaps
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533 FELIVRFNQLDVIARNAYLLNCA-------WALISLIILFAAIAVGRETK 575
                                                                                                                                                                                                                                                                                               301;
                                  Length 756;
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                                  ; Score 237.5; DB 4;
; Pred. No. 3.5e-13;
89; Mismatches 232;
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                                   4.18;
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                                                          Conservative
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; OTHER INFORMATION:
US-09-147-236-3
                                                          Matches 156;
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US-08-960-048-9
                                   Query Match
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d. No. 2.5e-
Mismatches
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Window
SEQ ID NO 9
                                                                   ; TYPE: PRT
; ORGANISM: Acetobacter xylinu
US-08-960-048-9
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; GENERAL INFORMATION:
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                                                                                                                                                                     Matches 154; Conservative
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                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                           187 LDDG-----
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PCT-US91-01726-4
                                                 LENGTH: 723
                                                                                                                                     Query Match
                                                                                                                                                       Best Local
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989 NMVGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGL-MGRQ-----NRTP 1040
                                                                                                                                                                                                                                                                                                      468 VYETTMALFLVRVTIVTLLSPSRGKFNVTDKGGLLEKGYFDLG-----AVYPNIILGL 520
                                                                                                                                                                                                                                                                                                                                                                                            365 LHIGORVRWARGMLQI-FRIDNPL---FGRGLSWGQRLCYLSAMISFLFAVPRVIFLSSP 420
                                                                                                                                                                                                           754 HVISCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSVYCMPKRPAFKGSAPINLS 813
                               320 EQIG------GFATQTVTEDAHTALKMQRLGWSTAYL--RIPLAGGLATERLI 364
                                                                                                                                                                                874 AICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVG----IDEWWRNEQFW-V 928
                                                                                                                                                                                                                                                                         929 IGGISAHLFAVFQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILII 988
                                                                                        814 DRINQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTTIYPLTSLPLLVYCILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Choi, Janice Y.
APPLICANT: Lei, Ke-Jian
APPLICANT: Lei, Ke-Jian
APPLICANT: Shelly, Leslie L.
TITLE OF INVENTION: GLUCOSE-6-PHOSPHATASE: THE GENE AND
TITLE OF INVENTION: PROTEIN AND RELATED MUTATIONS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Petentin Release #1.0, Version #1.25
SOFTWARE: Petentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,773
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNET/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 15280-175
REFERENCE/DOCKET NUMBER: 15280-175
TELECOMDNICATION INFORMATION:
TELEPHONE: (415) 549-5600
TELEFAN: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..357
OTHER INFORMATION: /label= R to C at 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08119773
; Patent No. 5460942
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NYIARPT----NEHAKAGNLNYAIG----HTDGDYILIFDCDH-VPTRAFL 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 VLRLVVLSIFLHYRLTNPVRNAYPLWL-----LSVICEIWFALSWILDQFPKWFPINRE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 TYLDRLALRYDREGEPSQLAAVDIFVSTVDPLKEPPIVTANTVLSILAVDYPVDKVSCYV 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P----LPL----PPNPDEWPTVDIEVPTYN---EELSIVRLTVLGSLGIDWPPEKVRVHI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 SDDGASMLTFDALAETSEFARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDR 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 REAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFFDINLRGLDGIQGPVYVGT 633
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            APPLICANT: Saxena, Inder M
APPLICANT: Lin, Fong C
TITLE OF INVENTION: Recombinant Cellulose Synthase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01726
FILING DATE: 19910314
CLASCHTRIANGARYAN.
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                                                                                                                          ADDRESSEE: David L. Parker
STREET: 600 Congress Avenue Suite 2300
CITY: Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 494093
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARKET MY, DAY'IG L
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
Brown, Malcolm R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 723 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                            COUNTRY: United States ZIP: 78701
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                                                                                                                                                                                                           Texas
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PCT-US91-01726-4
APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

us-09-900-237-30.rai

sequence mutated ,	Length 357; Gaps 16: Autohatch 108: Autohatch	810 QY 66	65	867 UY OF 105		CLNVILWLGFWANQL 164 Qy 221 IPMT -FOFWVIGGISAHLF 937		Qy 280 VLRI FKWTTLLIDPTTLIINMVGVVAGT 997 :: : Db 610 AMSVWWHIDTTPFASILKNL-GTLEGL 271	1048 Qy 339	656	UY 390 DGA2	Qy 446 QPSF	Db 737 VTVS	07 506 LGHS	1:1: 1:1: 180 IGNS	- oy 561 Lp	Db 811 EDYG	Qy 580 LMDF	Db 871 LTVM	Qy 629		Qy 662 GGKK	Db 973 NLTK	Qy 710	DP 1033 EQLE	Qy 742 SSTE		782	Db 1145 KTCY
); OTHER INFORMATION: /note= "The G-6-Pase amino acid; OTHER INFORMATION: from Arg to Cys at position 83. US-08-119-773-4	Query Match 2.0%; Score 114; DB 1; Le Best Local Similarity 19.1%; Pred. No. 0.043; Matches 72; Conservative 59; Mismatches 137:	EALHVISCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSV	Db 14 QSTHYLQVNYQDSQDWFILVSVIADLRNAFYVLFPIWFHLQEAVGIKLLMVA	QY 811 NLSDRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTTIYPLTSLPLL- :	868	DD 106 PVICETGPGSPSGHAMGTAGVYYVMVISTLSIFQGK-IKPIYRFRCLNVILWLGFWAVQL OV 889 - NLASIWFIALFFISIFAATGILEMRWSGVGIDEWWRNFOFWVIGGISAHLF	165 NVCLSRIYLAAHPPHQVVAGVLSGIAVTETFSHIHSIYNAS	OY 938 AVEGGLLKVLAGIDINFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINMYGVVAGT :	998 SYAINSGYQSWGPLFGKLFFAFWVIV	Db 272 GLALNSSMYRESCKGKLSKWLPFRLSSIVASLVLLHVFDSLK	Qy 1049 LLASIFSLIMVRVDPF 1064 ::: Db 328 CKRAVVPLASVSVIPY 343		RESULT 12 HG-08-660-668-8	.; Sequence 8. Application US/08669656A	; GENERAL INFORMATION: ; GENERAL INFORMATION: abblicant wood John N	APPLICANT: AKOPIAN, Armen N. MINTED OF INVENTION 100 CO.	NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS:	: STREET 1800 Concord Pike. P.O. Rox 15437	CITY: Wilmington	COUNTRY: USA	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	(V)	SOFTWARE: Patentin Release #1.0, Version #1.25; CURRENT APPLICATION DATA:	; APPLICATION NUMBER: US/08/669,656A : FILING DATE: 24-7UN-1996		NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712	; REFERENCE/DOCKET NUMBER: PHM.70086 ; TELECOMMUNICATION INFORMATION:	; TELEPHONE: (302) 886-7466 ; INFORMATION FOR SEQ ID NO: 8:	<pre>; SEQUENCE CHARACTERISTICS; ; LENGTH: 1957 amino acids</pre>

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LAPYLGESWKRKDSPQVPAEGVDDTSSSEGSTVD 1092 EGCTRRCPCCNVNTSKSPWAT--GW-----QVR 1144 DDGSDFNYPASGTEDQKQKIADRMRSWRMNTGG 120 |:: | :: | : : : : : | CITPDDGVFHGDQESRRGSILLGRGAGQTGPLP 550 -----CDHYINN----SKAVREAMC---F 579 ASFLVVFRILCGEWIENMWVCMEVSQKSICLILF 870 LEKREGOS-----AAFVASTLMEYGGVPQ 741 AP----INLSDRLNQVLRWALGSVEILFSRHCP 836 LAFEDNYLEEKPRVKSVLEYTDRVFTFIFVFEML 1204 PLTSL--PLLVYCILPAICLL-----TG 880 GLSKYD----SGEIPRGYVPSVTNSQMSGEIP 162 MEDALLNDETROPLSRKVPIASSKIN-PYRMVI 279 -----DITG----KSFLSAGYLNEPFRAQR 609 ARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKV 445 RYANRNTVFFDINLRGLDGIQGP------ 628 ----IALLLNSFSADNLTAPEDDGEVNNLQL 912 NRTAI---YGYEPPIKAKK-----PGFLASLC 661 VPV----FNLEDIEEGVEGAG-----FDDEK--- 709 E------DKSEWGTEIGWIYGSVTEDI 781 PNPSREF -- SGSIGNVAWKERVDGWKMKQDKGA 220 LSVICEIWFALSWIL-DQFPKWFPINRETYLDR 338 KEPPI---VTANTVLSILAVDYPVDKVSCYVSD 395 SKALKVPEEGWIMQDGTPWPGNNTRDHPGMIQVF 505 IRSLRLLR --- VFKLAKSWPTLNT ----LIKI - 779 SFQHHKKAGAMNALVRVSAVLT-----NGQYMLN 560 re 112; DB 4; Length 1957; ed. No. 1.2; Mismatches 371; Indels 450; OSHSGSPLASKNANERRP GRRRASHGSVFHFRAPSQI THRETSIAPSEGRAATDID **LLVVLSIFLHYRLTNPVRN** SVVSI -----MTSVIEE RYDREGEPSQLAAVDIFV 国伍-----||||: ---AFDAMLQAGNIVFTV SFVKDRRAMKREYEEFKIR ISGGLDTEGNELPRLVYVS GCRKDGVSVWNGEKLRWH ----VXVG ----SGNVGHPKYDSG PDHHMMSPTGNISRRAPF -----RSPL PNLGPQVCYVQFPQRFDG ARIQVLGHRASRAIASYIS KPALSSPKENHGDFITDP TAS-----: : .PQVQKCENHQAARSPASM PEETLRKIPELADDLDER YRIVEHSWFESFILFMIL WYGYGGRLKFLERFAYINT | || : | : ::: SMLTFDALAE-----KKASKSKKRSSDKKKSN SFKMHARGWRSVYCMPKRE SLLELSASKKG-----|: || || | |GELTAGAP-EGPAL---KRHRGSPAIRGEEGD--PESLLKEAIHVI ----Similarity 17.5 07; Conservative MVLGNLVVLNLF----TYPE: protein ----St

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                                                                                                                                       1205 LKWVAYGFKKYFTNAWCWLDFLIVNISLTSLIAKILEYSDVASIKALRTLRALRPLRALS 1264
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                                    KF------IMPEISNLASIWFIA-LFLSIFATGILEMRWSGV-----GID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATE: B4-10, Version #1.25
APPLICATION NUMBER: US/08/669,656A
FILING DATE: 24-10N-1996
CLASSIFECATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISSTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PHM.70086
TELECOMMONICATION INFORMATION:
TELECOMMONICATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                 1384 INSQPNWEN----NLYMYLYFVVFIIFGGFFTLNLFVGVI 1419
                                                                                                                                                                                       956 VTSKANDEEGDFAELYMFKWTTLLIPPTTILIINM-VGVV 994
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ADDRESSEE: ZENECA Pharmaceuticals
STREET: 1800 Concord Pike, P.O. Box 15437
                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08669656A
Patent No. 6451554
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Wood, John N.
APPLICANT: AROPLA, Armen N.
TITLE OF INVENTION: Ion Channel
NUMBER OF SEQUENCES: 31
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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LENGTH: 1957 amino acids
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MOLECULE TYPE: protein
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STATE: Delaware
COUNTRY: USA
                                                                                                              919 EWWRNEQ----
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280 VLRLVVLSIFLHYRLTNPVRNAYPLWLLSVICEIWFALSWIL-DQFPKWFPINRETYLDR 338
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APPLICANT: Payne, Jewel
APPLICANT: Narva, Kenneth E.
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US-08-485-568A-6
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DD 364 IDVLTPINTGIGFQESSDLRKF QY 561 LDCDHYINNSKAVREAMCFLMD	696 IEEGVEGACFDDEKSVLMSQ	OY 914 GVGIDEWWRNEQFWVIGGISAH SVFOGILKVLAGIDTNFTVTSKA	15 K
APPLICANT: Fu, Jenny M. TITLE OF INVENTION: No. 5589382el Bacillus thuringiensis Genes Encoding TITLE OF INVENTION: Nematode-Active Toxins VINDER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSE: David R. Saliwanchik STRE: 121N N. 4.18t Street, Suite A-1 CITY: Gainesville STATE: Florida COUNTRY: USA ILP: 32606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/485,568A FILING DATE: CLASSIFICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US 08/310,197 FILING DATE: 21-SEP-1994 CLASSIFICATION UNMBER: US 07/918,345 FILING DATE: 21-JUL-1992 CLASSIFICATION UNMBER: US 07/918,345 FILING DATE: 21-JUL-1992 CLASSIFICATION DATA: APPLICATION NUMBER: US 07/558,738 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 07/558,738	FILING DATE: 17-016-1990 CLASSTFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/357,698 FILING DATE: 16-DEC-1994 CLASSIFICATION DATA: APPLICATION NUMBER: 08/176,403 FILING DATE: 30-DEC-1993 CLASSIFICATION 08 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/7/999,053 FILING DATE: 14-JUL-1993 CLASSIFICATION DATA: APPLICATION NUMBER: 08/07/999,053 FILING DATE: 18-JUL-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: SAILWANGCHAK, DAVIG R. FEFERENCE/DOCKET NUMBER: 31,794 FEFERENCE/DOCKET NUMBER: 31,794 FEFERENCE/DOCKET NUMBER: 31,794 FEFERENCE/DOCKET NUMBER: 31,794 FEFERENCE/DOCKET NUMBER: 31,794	TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID No: 6: 5 SEQUENCE CHARACTERIZICS: LENGTH: 1167 amino acids TYPE: amino acid TYPE: amino acid TYPE: amino acid STANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-08-485-568A-6 Best Local Similarity 19.7%; Pred: No. 1.2; MAtches 139; Conservative 77; Mismatches 214; Indels 276; Gaps 36; Qy 411 EFARWVPFVKKYDIEPRADEFYECQKIDYLKDRVQPSFVKDRRAMKREYEE 1

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561 LDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQFPQRFDGIDRNDRYANR----- 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 EFARKw-----VPFVK--KYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      502 IQVFLGHSGGLD-TEGNELPRLVYVSREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLN 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESLLKEAIHV--ISCGYEDKSEWGTEIGWIYGSVTED-----ILTGFKMHARGWRSVYC 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 FKIRINALVSKALKV-------PEEGWIMQDGT------PWPGNNTRDHPGM 501
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19.7%; Pred. No. 1.2;
tive 77; Mismatches 214; Indels 276;
                                                                                                                                                                                                                                                                          PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/176,403
FILING DATE: 30-DEC-1993
CLASSIERCATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/999,053
FILING DATE: 14-ULL-1993
CLASSIERCATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: SALIWANCHIK, DAVIG R.
REGISTATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: MA48DD2.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,345
FILING DATE: 21-UL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,738
FILING DATE: 27-UL-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/357,698
FILING DATE: 16-DEC-1994
CLASSIFICATION: 435
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21-SEP-1994
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Matches 139; Conservative
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MOLECULE TYPE: protein
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STRANDEDNESS: sir
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                                                                                                                                           798 MPKRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTT 857
                                                                                          688 -LPSTSTP-----TSTNFVEPESLEKIINQVN----QLFSSSSQTEL---- 724
                                                              858 IYPLTSLPLLVYCILPAICLLTGKFIMPE----ISNLASIWFIALFLSIFATGILEMRWS
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Search completed: February 19, 2003, 16:37:43 Job time: 47 secs

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February 19, 2003, 16:36:16; Search time 31 Seconds (without alignments) 890.090 Million cell updates/sec
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1 MDGDADALKSGRHGAGDVCQ......VDPFTTRLAGPNIQTCGINC 1080
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140259 seqs, 25548876 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                       - protein search,
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Perfect score:
Sequence:
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                                                                                                                    protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 30, Appl	33,	8, A	26,	8,	14,	Sequence 10, Appl	4	Sequence 6, Appli	32	18	24,	31, 7	7, A	20,	16,	28,	6, A	7
	ΙD	US-09-900-237-30	US-09-900-237-33	US-09-838-539-8	US-09-900-237-26	US-09-900-237-8	US-09-900-237-14	US-09-900-237-10	US-09-900-237-4	US-09-838-539-6	US-09-900-237-32	US-09-900-237-18	US-09-900-237-24	US-09-900-237-31	US-09-838-539-7	US-09-900-237-20	US-09-900-237-16	US-09-900-237-28	US-09-900-237-6	US-09-900-237-2
	DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	Query Match Length DB	1080	1065	881	1091	1165	1039	1086	1148	974	701	793	740	685	685	206	610	431	320	304
ф	Query	100.0	78.0	77.1	9.69	66.5	66.1	66.1	66.1	60.2	58.9	56.0	52.6	48.7	48.7	46.5	45.5	35.4	24.6	23.9
	Score	5778	4507	4455.5	4021.5	3844.5	3820.5	3818	3818	3477	3404.5	3234	3038.5	2816	2811	2689	2627.5	2044.5	1418.5	1379.5
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CLQCKTKYKRHRGSPAIRGEEGDDTDADDGSDFNYPASGTEDQKQKIADRMRSWRMNTGG 120 SGNVGHPKYDSGEIGLSKYDSGEIPRGYVPSVTNSQMSGEIPGASPDHHMMSPTGNISRR

61

δ g δλ qq QY

121 121 181

120 180 APFPYVNHSPNPSREFSGSIGNVAWKERVDGWKMKODKGAIPMINGTSIAPSEGRAAIDI 240

Sequence 22, Appl Sequence 12, Appl Sequence 15, Appl Sequence 16, Appl Sequence 11, Appl Sequence 11, Appl Sequence 10, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 22, Appl Sequence 24,	; Gaps 0;	TQA 60
Sequence	Length 1080 Indels 0;	/CRPCYEHERKEG CRPCYEHERKEG
340 10 US-09-900-237-12 165 10 US-09-734-569-154 165 10 US-09-734-569-154 165 10 US-09-734-569-138 115 10 US-09-734-569-138 115 10 US-09-734-569-138 115 10 US-09-734-569-132 12 10 US-09-818-539-13 12 10 US-09-818-539-13 12 10 US-09-818-539-13 13 10 US-09-818-539-13 13 10 US-09-818-539-13 13 10 US-09-818-539-13 13 10 US-09-818-134 13 10 US-09-818-134 13 10 US-09-815-24 143 10 US-09-815-24 144 10 US-09-818 113 10 US-09-818 114 10 US-09-818 114 10 US-09-818 114 10 US-09-818	100.0%; Score 5778; DB 10; .larity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0;	MDGDADALKSGRHGAGDVÇQICADGLGTTLDGDVFTACDVCRFPVCRPCREHERKEGTQA
20 1162.5 20.1 340 10 22 23 501 8.9 160 341 10 23 501 8.7 156 10 24 476.5 8.2 165 10 26 26 4.9 115 10 26 26 28 4.6 693 115 10 29 20 20 20 20 20 20 20 20 20 20 20 20 20	atch cal Simi 1080;	1 MDGDADALKSG
RESULT 1 RESULT	Query M Best Lo Matches	da d

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Gaps

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Length Indels

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DB

FDALAETSEFARKWVPFVKKYDIEPRAPEFYFC 435 EGAGFDDEKSVLMSQMSLEKRFGQSAAFVASTL 733 EDKSEWGTEIGWIYGSVTEDILTGFKMHARGWR 793 RPCYEHERKEGTQACLQCKTKYKRHRGSPAIR 78 QKIADRMRSWRMNTGGSGNVGHPKYDSGEIGLS ASPDHHMMSPTGNISRRAPFPY - VNHSPNPSRE MINGISIAPSEGRAATDIDASTEYNMEDALLND :: | || | | | |||||||| ::|||||||||||---STQAASE-RGGVDIDASTDILADEALLND LVVLSIFLHYRLTNPVRNAYPLWLLSVICEIWF /YVSREKRPGFQHHKKAGAMNALVRVSAVLTNG GYEPPIKA--KKPGFLASLCGGKKKASKSKRR KFIMPEISNLASIWFIALFLSIFATGILEMRWS FKIRINALVSKALKVPEEGWIMQDGTPWPGNNT PNLGPQVCYVQFPQRFDGIDRNDRYANRNTVFF IDREGEPSQLAAVDIFVSTVDPLKEPPIVTANT RWALGSVEILFSRHCPLWYGYGGRLKFLERFAY Mismatches 107; 4507; No. 0; re / PRIOR APPLICATION NUMBER: 09/ PRIOR FILING DATE: 2000-12-21 NUMBER OF SEQ ID NOS: 33 SOFTWARE: MICTOSOFT OFFICE 97 78.0%; 78.4%; ETRQPLSRKVPIASSKINPYRM | |||||||| | ||:||||||| EARQPLSRKVSIPSSRINPYRM ORGANISM: Arabidopsis thalia 79 GEEGDDTDADDGS-DFNYPASG 138 KYDSGEIPRGYVPSVTNSQ-MS ----EVSHNHLPRLTSRODTS FSGSIGNVAWKERVDGWKMKQD ALSWILDQFPKWFPINRETYLD 299 ALSWILDQFPKWFPVNRETYLD VLSILAVDYPVDKVSCYVSDDG QKIDYLKDKVQPSFVKDRRAMK GDHPGMIQVFLGQNGGLDAEGN DINERGEDGIQGPVYVGTGCVF SSDKKKSNKHVDSSVPVFNLED INTTIYPLTSLPLLVYCILPAI CQICADGLGTTLDGDVFTACDV 20 CQICSDNVGKTVDGDRFVACDI VLSILAVDY PVDKVSCYVFDDG RDHPGMIQVFLGHSGGLDTEGN 556 QYMLNLDCDHYINNSKAVREAM DINLRGLDGIQGPVYVGTGCVF MEYGGVPQSSTPESLLKEAIHV SVYCMPKRPAFKGSAPINLSDR SIYCMPKLPAFKGSAPINLSDR 419 AKIDYLKDKVQTSFVKDRRAMN ESDKKKSGRHTDSTVPVFNLD Conservative Similarity LENGTH: 1065 TYPE: PRT US-09-900-237-33 836; SEQ ID NO 33 Query Match Best Local S Matches 836 80 196 183 256 239 316 359 436 496 599 629 734 719 854 376 919 674 794

495

555 538 615 598 673 658 853

913

315

298 375

195

137

099

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980 IPPTTILIINMVGVVAGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLMGRQNRT 1039
                                                                                                                                                                    NISRRAPFPYVN-HSP-----NPSREF-SGSIGNVAWKERVDGWKMKQDKGAIPMTNG 226
                                                                                                                                                                                                            WWRNEQEWVIGGISAHLFAVFQGLLKVLAGIDINFTVTSKANDEEGDFAELYMFKWTTLL 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LQCKTKYKRHRGSPAIRGEEGDDTDADD-GSDFNYPASGTEDQKQKIADRMRSWRMNTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SGNVGHPKYDSGEIGLSKYDSGEIPRGYVPSVTNS-OMSGEIPGASPDHHMM----SPTG 175
                                                                                                                                                                                                                             POSSTPESLLKEAIHVISCGYEDKSEWGTEIGWIYGSVTEDILTGFKMHARGWRSVYCMP
                                                      800 KRPAFKGSAPINLSDRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTTIY
                                                                                                             860 PLTSLPLLVYCILPAICLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVGIDE
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                                                                                                                                                                                                                                                                                                                           1040 PTIVIVWAVLLASIFSLLWVRVDPFTTRLAGPNIQTCGINC 1080
                                                                                                                                                                                                                                                                                                                                           GENERAL INCOMPATION.

APPLICANT: Allen, Stephen
TITLE OF INVENTION: Plant Cellulose Synthases;
FILE REFERENCE: BB170 US CIP
CURRENT APPLICATION UNMER: US/09/900,237
CURRENT FILING DATE: 2001-07-06
PRIOR PPLICATION NUMBER: 60/92,844
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-13
PRIOR RILING DATE: 1998-07-13
PRIOR APPLICATION NUMBER: 09/720383
PRIOR APPLICATION NUMBER: 09/720383
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 69.6%; Score 4021.5; Best Local Similarity 68.1%; Pred, No. 0; Matches 749; Conservative 138; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 26, Application US/09900237; Patent No. US20020120124A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Impatiens balsamia
US-09-900-237-26
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GVGIDEWWRNEQFWVIGGISAHLFAVFQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMF
               Length 881;
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                                                                                                                                                                                                                                                 TILE OF INVENTION: Plant Cellulose Synthase and Prontite OF INVENTION: Plant Cellulose Synthase and Prontite OF INVENTION: Sequences
TITLE OF INVENTION: Sequences
CURRENT APPLICATION NUMBER: US/09/838,539
CURRENT FILING DATE: 1001-04-18
PRIOR FILING DATE: 1996-10-29
PRIOR PRILING DATE: 1997-10-29
PRIOR FILING DATE: 1997-10-29
NUMBER OF SED ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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93.4%; Pred. No. 0;
iive 39; Mismatches
                                                                                                                                                                                                            Sequence 8, Application US/09838539 Patent No. US20020129401A1 GENERAL INFORMATION:
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US-09-838-539-8
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Best Local Similarity
Matches 823; Conserv
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US-09-838-539-8
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Gaps 61

MVIVLRLVVL 286 : : :: VVIILRLIIL 298	DRLALRYDRE 346 :: DRLSMRFDRE 358	GASMLTFDAL 406 :: : GSAMLTFEAL 418	KREYEEFKIR 466 KREYEEFKVR 478	NELPRLVYVS 526 NELPRLVYVS 538	MCFLMDPNLG 586 : EMMDPNLG 598	FNRTAIYGYE 646 : : FNRQALYGYD 658	EDIEEGVEGA 703 : EDIEEGIE 716	HVISCGYEDK 763 HVISCGYEDK 775	DRLNQVLRWA 823 DRLNQVLRWA 835	AICLLTGKFI 883 AICLLTGKFI 895	AHLFAVFQGL 943 AHLFAVFQGL 955	VAGTSYAINS 1003 : VAGVSFAINS 1015	FSLLWVRVDP 1063 FSLLWVRIDP 1075		
'TSIAPSEGRAATDIDASTEYNMEDALLNDETRQPLSRKVPIASSKINPYRMVIVLRLVV: : : : : : : : : : : : :	SIFLHYRLTNPVRNAYPLMLLSVICEIWFALSWILDQFPKWFPINRETYLDRLALRYDRE	GEPSQLAAVDIFVSTVDPLKEPPIVTANTVLSILAVDYPVDKVSCYVSDDGASMLTFDAL	AETSEFARKWVPEVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKIR 	INALVSKALKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYV.		PQVCYVQFPQRFDGIDRNDRYANRNIVFFDINLRGLDGIQGPVYVGTGCVFNRTALY\ :	PPIKAKKPG-FLASLCGGKKKASKSKKRSSDKKRSNKHVDSSVPVFNLEDIEEGVEGA	GFDDEKSVLMSQMSLEKRFGQSAAFVASTLMEYGGVPQSSTPESLLKEAIHVISCGYEDK -	SEWGTEIGWIYGSYTEDILTGFKMHARGWRSYCMPKRPAFKGSAPINLSDRLNQYLRWA :	LGSVEILFSRHCPLWYGYGGRLKFLERFAYINTIYPLTSLPLLYCLLPAICLIGGRF. :	MPEISNLASIWFIALFLSIFATGILEMRWSGVGIDEWWRNEQFWVIGGISAHLFAVFQGL 	LKVLAGIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINWVGVVAGTSYAINS	GYOSWGPLFGKLFFAFWVIVHLYPFLKGLMGRQNRTPTIVIVWAVLLASIF	FTTRLAGPNIQTGGINC 1080 	ESULT 5 209-900-237-8 Sequence 8, Application US/09900237 Sequence 8, Application US/09900237 Patent No. US20020120124A1 GENERAL INFORMATION: APPLICANT: Allen, Stephen TITLE OF INVENTION: Plant Cellulose Synthases FILE REFERENCE: BB1170 US CIP CURRENT APPLICATION NUMBER: US/09/900, 237 CURRENT FILING DATE: 2001-07-06 PRIOR FILING DATE: 1998-07-14
227	287	347	407	467	527	587	647	704	764	824	884 896	944	1004	1064	SULT 5 -09-900. Sequence Patent 1 GENERAL APPLICY TITLE CURRENT CURRENT PRIOR 1
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FGQSSVFVASTLLENGGTLKSASPASLLKEAIHV 840
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|SLAAYGYGSVAWKERMEGWKQKQER-----L 309
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                                                                                                                    bre 3844.5; DB 10; Length 1165;
2d. No. 1.1e-317;
Mismatches 175; Indels 69;
  /15871
PRIOR APPLICATION NUMBER: PCT.
PRIOR FILING DATE: 1999-07-13
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 1165
                                                                                                                    Query Match
Best Local Similarity 65.4%
Matches 723; Conservative
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364 FFFHYRVMHPAKDAFALWLIS
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                                                                             TYPE: PRT
CORGANISM: Zea mays
US-09-900-237-8
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                                                                                                                                                                   488 TPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVYVSREKRPGFQHHKKAGAMNALVR 547
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SIICEIWFAFSWILDQFPKWFPIDRETYLDRLSIRYEREGEPNMLAPVDVFVSTVDPMKE 344
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TITLE OF INVENTION: Plant Cellulose Synthases
TITLE OF INVENTION: Plant Cellulose Synthases
FILE REFERENCE: BB1170 US CIP
CURRENT APPLICATION NUMBER: US/09/900,237
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/092,844
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1999-07-17
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 2000-12-21
NUMBER OF ED IN ONS: 33
SOFTWARE: MICROSOFT Office 97
FRED IN ON 10
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Patent No. US20020120124A1
; GENERAL INFORMATION:
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ORGANISM: Zea mays
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 192 PSR----EFSGSIGNVAWKERVDGWKMKQDKGAIPMTNGTSIAPSEGRAATDIDASTEYN
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                                                  CLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVGIDEWWRNEQFWVIGGISAH
                                                                                                                  LFAVFQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTT1LI1NNVGVVA
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                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/09900237
Patent No. US200201201241
GENERAL INFORMATION:
APPLICANT: Allen, Stephen
TITLE OF INVENTION: Plant Cellulose Synthases
FILE REFERENCE: BB1170 US CIP
CURRENT APPLICATION NUMBER: US/09/900,237
CURRENT APPLICATION NUMBER: US/09/900,237
FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: QV/092,844
PRIOR APPLICATION NUMBER: QV/092,844
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 2000-12-1
NUMBER OF SEQ ID NOS: 33
SOFTWARE: MICROSOFT Office 97
                                                                                                                                                                                                                                                   1056 LLWVRVDPFTTRLAGPNIQTCGINC 1080
                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine
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NAME/KEY: UNSURE
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Best Local S:
Matches 719
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us-09-900-237	0-237-10	TADA TADA DA
Query Match Best Local	uery Match 66.1%; Score 3818; DB 10; Length 1086; est Local Similarity 64.7%; Pred, No. 1.8e-315; atches 716; Concentration 141; Mismarches 178; Indels 72; Cane 17.	999 VAGVSNAINNGYESWGPLF
^0	DGDADALKSGRHGAGDVCOLCADGLGTTLDGDVCTACDVCRFPVCRPCYEHERKEGTOAC 61	OY 1054 FSLLWVRVDPFTTRLAGPNIOT
8		Db 1059 FSLLMVRIDPFLAKDDGPLLE
Oy 62 Db 82	! LQCKTKYKRHRGSPAIRGEEGDDTDADDGSDFNYPASGTEDQKQKIADRMRSWRMNTGGS 121	RESULT 8 US-09-900-237-4 ; Sequence 4, Application US/099
12	GNVGHPKYDSGEIGLSKYDSGEIPRGYVPSVTNSQMSGEIPGASPDHHMMSPT	; Patent No. USZU0Z01Z01Z4A1 ; GENERAL INFORMATION: ; APPLICANT: Allen, Stephen
12	YGHMSYGRGGDP	; TITLE OF INVENTION: Plant Ce. ; FILE REFERENCE: BB1170 US CIR. CIRDERM AND INVENTION MINDER.
UY 1/3 Db 178	GNISKRAFFFYNHSPNDRSESG-SLEWYAMEKWCWGMARAKDKAALPMIN GGGGKRIHPLPYADPSLPVQPRSMDPSKDLAAYGYGSVAMKERWENWKQRQERMHQTG	CURRENT APPLICATION NUMBER: CURRENT FILING DATE: PRIOR APPLICATION NUMBER: 60,
Oy 226 Db 236		FRIOR FILLING DAIE: 1990-01-1; PRIOR FILLING DATE: 1999-07-1; PRIOR FILLING DATE: 0999-07-1; PRIOR APPLICATION NUMBER: 09
Oy 286 Db 283	5 LSIFLHYRLTNPVRNAYPLMLLSVICEIWFALSWILDOFPKWFPINRETYLDRLALRYDR 345 	PRIOR FILING DATE: 2000-1. NUMBER OF SEQ ID NOS: 33 SOFTWARE: Microsoft Offic. SEQ ID NO 4
Qy 346 Db 343	 5. EGEPSQLAAVDIEVSTVDPLKEPPIVTANTVLSILAVDXPVDKVSCTVSDDGASMLTFDA 405 14:1111 : 1 11111111111111111111111111	; LENTH: 1148 ; TYPE: PRT ; ORGANISM: Zea mays US-09-900-237-4
Qy 406 Db 403	5 LABTSEFARKWVPFVKKYDIEPRAPEFYFCQKIDYLKDKVQPSFVKDRRAMKREYEEFKI 465 	Query Match 66.1% Best Local Similarity 65.1% Matches 714; Conservative
Qy 466 Db 463	S RINALVSKALKVPEBGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTBGNBLPRLVVV 525 	Qy 16 GDVCQICADGLGTTLDGDVFT Db 95 GQVCQICGDDVGRNPDGEPFV
QY 526 Db 523	S SREKRPGFQHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYINNSKAVREAMCFLMDFNL 585 	Qy 76 AIRGEEGDDTDADDGSDFNYF :
Qy 586 Db 583	5 GPQVCXVQFPQRFDGIDRNDRYANRNTVFFDINLRGLDGIQGFVYVGTGCVFNRTAIYGY 645 	Qy 130 DSGBIGLSKYDSGELPRGYVF
Qy 646 Db 643	5 EPPIKAKKPGFLASLCGGKKRASKSKKRSSDKKKSNKHVDSSVPVFNL 693 	Qy 187 NHSDNPSREFSG-S : : :: Db 251 DPNLPVQPRSMDPSKDLAAYG
Oy 694 Db 702	EDIEBGVEGAGFDDEKSVLMSQMSLEKRFGQSAAFVASTLMEYGGVPGSSTPESLLKEAI 753 	QY 239 DIDASTEYNMEDALLNDETRC Bb 303 GDDADLPLMDEARC
Qy 754 Db 760	1 HVISCGYEDKSEWGTEIGWIYGSVTEDILTGFKWHARGWRSVYCMPKRPAFKGSAPINLS 813 	Qy 299 RNAYPLWLLSVICEIWFALSF : : :
Qy 814 Db 820	1 DRLNQVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTTIYPLTSLPLLVYCILP 873 	Oy 359 VSTVDPLKEPPLVTANTVLS:
Qy 874 Db 880	1 AICLLJGKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVGIDEWWRNEQFWVIGGIS 933 	QY 419 FVKKYDIEPRAPEFFCGKI 476 FCKRYSLEPRAPEWYFQQKI
Qy 934 Db 940	1 AHLEAVFQELLKVLAGIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINWGV 993 	QY 479 EEGWIMQDGTPWPGNNTRDH

16; PVDKVSCYVSDDGASMLTFDALAETSEFARKWVP 418 PRWFPINRETYLDRIALRYDREGEPSOLAAVDIF 358 RFPYCRPCYEHERKEGTQACLQCKTKYKRHRGSP 75 ||:|| ||:||:||:|| || || ||:|| :| |AFPICRDCYEYERREGTQNCPQCKTRFKRLKGCA 154 DOKOKIADRMRSWRMNTGGSGNVG-----HPKY 129 | : | | | : | | HDSQYLAESMLHAHMSYGRGADLDGVPQPFHP-- 209 OMSGEIPGASPDHHMMSPT---GNISRRAPFPYV 186 WKERVDGWKMKQDKGAIPMTNGTSIAPSEGRAAT 238 |||||::|| ||:::| |WKERMESWKQKQER--MHQTR-----NDGGGDD 302 (VPIASSKINPYRMVIVLRLVVLSIFLHYRLTNPV 298 :|: ||:|||||||:|::||||| | |||:::|| IPLPSSQINPYRMIIIIRLVVLCFFFFHYRVMHPV 355 VQPSFVKDRRAMKREYEEFKIRINALVSKALKVP 478 ore 3818; DB 10; Length 1148; ed. No. 2e-315; Mismatches 168; Indels 74; Gaps se Synthases 7900,237 9/15871 1080 1085 44

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| Patent No. US20020129401A1
| GENERAL INFORMATION:
| APPLICANT: Stalker, D. et al. |
| TITLE OF INVENTION: Plant Cellulose Synthase and Promoter: | TITLE OF INVENTION: Sequences |
| TITLE OF INVENTION: Sequences |
| TITLE OF INVENTION: Sequences |
| FILE REFERENCE: 15621/03/US |
| CURRENT FILING DATE: 2001-04-18 |
| PRIOR APPLICATION NUMBER: 60/029,987 |
| PRIOR APPLICATION NUMBER: 60/029,987 |
| PRIOR APLICATION NUMBER: 08/960,048 |
| PRIOR FILING DATE: 1997-10-29 |
| NUMBER OF SEX ID NOS: 12 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
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1larity 61.5%; Pred. No. 1.4e-286;
Conservative 129; Mismatches 176;
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                       SKYDSGEIPRGYVPSVTNSQMSGEIPGASPDHHMMSPTGNISRRAPFPYVNHSPNPSREF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INLRGLDGIQGPVYVGTGCVFNRTAIYGYEPPIKAKKPGFLASLCGGKKKASKSKKRSSD
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KWTTLLIPPTTILIINMVGVVAGTSYAINSGYQS 1007 535 243 595 SVGIDEWWRNEOFWVIGGISAHLFAVFOGLLKVL 947 827 887 OFPKWFPINRETYLDRLALRYDREGEPSQLAAV 355 DYPVDKVSCYVSDDGASMLTFDALAETSEFARK 415 DKVQPSFVKDRRAMKREYEEFKIRINALVSKAL 475 SEDKKKSNKHVDSSVPVFNLEDIEEGVEGAGFDD 707 JEYGGVPQSSTPESLLKEAIHVISCGYEDKSEWG 767 Gaps QVFLCHSGCLDTEGNELPRLVYVSREKRPGFQH CDHYINNSKAVREAMCFLMDPNLGPQVCYVQFP INTTIYPLTSLPLLVYCILPAICLLTGKFIMPEI 14; Length 793; Indels bre 3234; DB 10; ed. No. 4.4e-266; Mismatches 87; e Synthases 900,237 /15871 ADDITIONAL ALLEN, Stephen TITLE OF INVENTION: Plant Cell FILE REFERENCE: BBI170 US CIF CURRENT APPLICATION NUMBER: COURRENT FILING DATE: 1998-07-14 PRIOR FILING DATE: 1998-07-14 PRIOR FILING DATE: 1999-07-14 PRIOR FILING DATE: 1999-07-15 PRIOR APPLICATION NUMBER: CF PRIOR FILING DATE: 2000-12-21 NUMBER: OF SEQ ID NOS: 33

SEQ ID NO 18 56.0% 73.3% Sequence 18, Application US/09 Patent No. US20020120124A1 GENERAL INFORMATION: QRFDGIDRHDRYSNRNVVFFD 296 NPVRNAYPLWLLSVICEIWFA 4 HPVNDAYGLWLTSVICEIWFA 124 WVPFCKKYNIEPRAPEWYFGO KVPEEGWIMODGTPWPGNNTR 536 HKKAGAMNALVRVSAVLTNGO -----FLASLCGGKKKAS EKSVLMSQMSLEKRFGQSAAF |||: ::| |||||||| EKTSNLTQTKLEKRFGQSPVF 356 DIFVSTVDPLKEPPIVTANTV WVPFVKKYDIEPRAPEFYFCQ **ORFDGIDRNDRYANRNIVFFD** 364 KTCNCWPKWCCLCCGSRKKKN 768 TEIGWIYGSVTEDILTGFKMH 948 AGIDTNFTVTSKANDEEGDFA EILFSRHCPLWYGYGGRLKFI SNLASIWFIALFLSIFATGII Conservative ORGANISM: Glycine max US-09-900-237-18 à

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us-09-900-237-30.rapb

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GTSYAINSGYQSWGPLEGKLFFFAFWVIVHLYPFLKGLMGRQNRTFTIVIVWAVLLASIFS 1055
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                                                                                                                                QHHKKAGAMNALVRVSAVLTNGQYMLNLDCDHYINNSKAVREAMCFLMDPNLGPQVCYVQ 593
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                                                                                                                LFAVFQGLLKVLAGIDTNFTVTSKANDEEGDFAELYMFKWTTLLIPPTTILIINMVGVVA
CLLTGKFIMPEISNLASIWFIALFLSIFATGILEMRWSGVGIDEWWRNEQFWVIGGISAH
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74.0%; Pred. No. 1.1e-230;
iive 78; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/09900237
Fatent No. US20020120124A1
GENERAL INFORMATION
APPLICANT: Allen, Stephen
TITLE OF INVENTION: Plant Cellulose Synthases
FILE REFERENCE: Ball70 US CIP
CURRENT APPLICATION NUMBER: US/09/900,237
CURRENT FILING DATE: 2001-07-06
FRIOR APPLICATION NUMBER: 60/092,844
FRIOR APPLICATION NUMBER: PCT/US99/15871
FRIOR APPLICATION NUMBER: 09/720383
FRIOR FILING DATE: 1998-07-13
FRIOR FILING DATE: 1998-07-13
FRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: MICROSOft Office 97
LENGTH: 685
                                                                                                                                                                                                                                                 1056 LLWVRVDPFTTRLAGPNIQTCGINC 1080
                                                                                                                                                                                                                                                                  ; ORGANISM: Gossypium hirsutum
US-09-900-237-31
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US-09-900-237-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KEGKPSELAGLDIFVSTVDPMKEPPLITANTVLSILAVDYPVDKVTCYVSDGAAMLTFE 62
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                                                                  IRINALVSKALKVPEEGWIMQDGTPWPGNNTRDHPGMIQVFLGHSGGLDTEGNELPRLVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%; Score 3038.5; DB 1
74.1%; Pred. No. 1.6e-249;
ive 97; Mismatches 79;
                                                                                                                                                                                                                                                                       GENERAL LINCARDATION:
TITLE OF INVENTION: Plant Cellulose Synthases
FILE REFERENCE: BB1170 US CIP
CURRENT APPLICATION NUMBER: US/09/900,237
CURRENT FILING DATE: 2001-07-06
PRIOR PILLING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/092,844
PRIOR APPLICATION NUMBER: 9CT/US99/15871
PRIOR APPLICATION NUMBER: PCT/US99/15871
PRIOR FILING DATE: 1999-07-13
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
                                                                                                                                                                                                                             Sequence 24, Application US/09900237
Patent No. US20020120124A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Picramnia pentandra
US-09-900-237-24
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                                                                                                                LAGPNIQTCGINC 1080
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Db 301 LEEIEEGLEGYEE Qy 752 AIHVISCGYEDKSEK Db 359 AIHVISCGYEEKTEK Qy 812 LSDRLNQVLRWALGS Qy 11 LSDRLHQVLRWALGS Qy 872 LPAICLLTGKFIMP Db 479 IPAVCLLTGKFIIP Db 479 IPAVCLLTGKFIIP Db 539 VSAHLFAVFQCLLKV Qy 992 GVVAGTSYAINSGYC Db 598 GVVAGTSYAINSGYC Db 598 GVVAGTSYAINSGYC Db 598 GVVAGTSYAINSGYC Db 598 GVVAGTSYAINNGYC Db 698 GVVAGTSYAINNGYC DC 698 GVVAGTSVAINNGYC DC	658 SULT 15 -09-900 Sequence Ratent 1 Ratent 1 APPLICA TITLE CURRENT CURRENT PRIOR 1 PRIOR 1 PRIOR 1 PRIOR 1 PRIOR 1 PRIOR 2 PRIOR 1 PRIOR 3 SEGIWARA	s kakakaka
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	RESULT 14 US-09-838-539-7 Sequence 7, Application US/09838539 Sequence 7, Application US/09838539 Patent No. US2020129401A1 GENERAL INFORMATION: APPLICANT: Stalker, D. et al. TITLE OF INVENTION: Plant Cellulose Synthase and Promoter TITLE OF INVENTION: Sequences FILE REFERENCE: 15621/03/US CURRENT APPLICATION NUMBER: US/09/838,539 CURRENT FILING DATE: 2001-04-18 PRIOR FILING DATE: 1996-10-29 PRIOR FILING DATE: 1996-10-29 PRIOR FILING DATE: 1997-10-29 NUMBER OF SEQ ID NOS: 12 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7 LENGTH: 685 TYPE: PRT VYPE: PRT ORGANISM: Gossypium hirsutum	Query Match 48.7%; Score 2811; DB 10; Length 685; Best Local Similarity 74.1%; Pred. No. 2.9e-230; Matches 509; Conservative 78; Mismatches 76; Indels 24; Gaps 413 ARRWVPEVKXYDIEPRAPEFYCQXIDYLXDKVQPSFVXDRAMKREYEEFKIRINALYS 472 1:11 11 11 11 11 11 11 11 11 11 11 11 11
	RESULT 14 Sequenc Sequenc Patent Patent APPLIC TITLE TITLE FILE R CURREN CURREN CURREN PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR SCOTWA SEQ ID LENGT L	Bess Bess Bess Bess Bess Bess Bess Bess

ô FWVIVHLYPELKGLMGRONRTPTIVIVWAVLLA 1051 |||||:||||||||||||||||||:||:||| FWVILHLYPPLKGLMGRONRTPTIVVLWSILLA 657 597 EDILTGEKMHARGWRSVYCMPKRPAFKGSAPIN 811 KANDEEGDFAELYMFKWTTLLIPPTTILIINMV 991 DRNDRYANRNTVFFDINLRGLDGIOGPVYVGTG 634 CGCKKRASKSKRSSDKKKSNKHVDSSVPVFNLE 694 LIGEKWHARGWRSVYCMPKRPAFKGSAPINLSD 814 EKRFGQSPVFIASTLMENGGLPEGTNSTSLIKE 358 FGQSAAFVASTLMEYGGVPQSSTPESLLKEAIH 754 Gaps ö re 2689; DB 10; Length 506; td. No. 4.2e-220; Mismatches 1; Indels 0 Synthases 900,237 /15871 1078 684 ø ||||| GSVEIFLSR | :||| |: PTLSNLTSV : || : LPKQTGPVL ion US/09 124Al ephen Plant Cel 170 US CIP NUMBER: U 2001-07 2001-07 998-07-14 MBER: PCI 999-07-13 MBER: 09/ 000-12-21 : 33 Office 97 TEIGWIYGS SELEKSTLM SVEILFSR EISNLASI PIKAKKPGE ||||||||||| PIKAKKPGE SWGTEIGWI TRLAGPNE 46.58 EKSVLMSON COSWGPLFG DACKVOFPC QVCYVQFPC EKSVLMSON CVLAGIDT aestivum vative

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        Qy
        815 RLNOVLRWALGSVEILFSRHCPLWYGYGGRLKFLERFAYINTTIYPLTSLPLLLVYCILPA

        Db
        241 RLNOVLRWALGSVEILFSRHCPLWYGGGRLKFLERFAYINTTIYPLTSLPLLVYCILPA

        301 RLNOVLRWALGSVEILFSRHCPLWYGGGRLKFLERFAYINTTYPLTSLPLLVYCILPA

        301 RLLTGKFIMPEISNLASIWFTALELSIFATGILEMRWSGVGIDEWWRNEOFWVIGGISA

        301 ICLLTGKFIMPEISNLASIWFTALELSIFATGILEMRWSGVGIDEWRNEOFWVIGGISA

        301 ICLLTGKFIMPEISNLASIWFTALELSIFATGILEMRWSGVGIDEWRNEOFWVIGGISA

        301 ICLLTGKFIMPEISNLASIWFTALELSIFATGILEMRWSGVGIDEWWRNEOFWVIGGISA

        302 HLFAVFOGILKVLAGIDTNFTYTSKANDEEGDFAELYMFKWTTLLIPPTTILINNVGVV

        401 HLFAVFOGILKVLAGIDTNFTYTSKANDEEGDFAELYMFKWTTLLIPPTTILINNVGVV
        420

        QY
        995 AGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLMGRQNRTPTIVIVWAVLLASIF
        1054

        Db
        421 AGTSYAINSGYQSWGPLFGKLFFAFWVIVHLYPFLKGLMGRQNRTPTIVIVWAVLLASIF
        480

        CQY
        1055 SLLWVRVDFFTTRLAGPNIQTGGINC
        506

        Db
        481 SLLWVRVDPFTTRLAGPNIQTCGINC
        506
```

Search completed: February 19, 2003, 16:41:44 Job time : 39 secs

